

BGS 201, Chlorina seedling 7, *fch7*

Stock number: BGS 201
Locus name: Chlorina seedling 7
Locus symbol: *fch7*

Previous nomenclature and gene symbolization:

Chlorina seedling 7 = *f7* (3).
Chlorina seedling 7 = *clo-f7^{f7}* (4).

Inheritance:

Monofactorial recessive (3).
Located in chromosome 1HL (3); about 4.7 cM proximal from the *trd1* (third outer glume 1) locus and about 22.7 cM distal from the *Blp1* (black lemma and pericarp 1) locus (3); *fch7.h* is associated with SNP markers 1_0911 to 1_1481 (positions 177.51 to 186.13 cM) in 1H bin 13 of Bowman backcross-derived line BW363 (1); likely in 1H bin 13.

Description:

Seedlings are light green and remain light green until near maturity (3). Plant vigor and seed yields are reduced, and developmental stages are delayed. Heading of plants in the Bowman backcross-derived line BW363 was delayed by up to 9 days compared to Bowman, but plant height was normal in most environments. Kernel weights were reduced by about 10% and grain yields were 85 to 95% of normal (2).

Origin of mutant:

A spontaneous mutant in Smyrna (PI 7969) (3).

Mutational events:

fch7.h (Smyrna II, GSHO 4) in Smyrna (3); *fch7.i* (Smyrna III) in Smyrna (PI 7969) (5).

Mutant used for description and seed stocks:

fch7.h (GSHO 4) in Smyrna; *fch7.h* in Bowman (PI 483237)*7 (GSHO 2058, BW363, NGB 20602).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Robertson, D.W. 1969. Linkage studies with five naturally occurring chlorophyll mutations in barley (*Hordeum* species). *Can. J. Genet. Cytol.* 9:321-326.
4. Simpson, D.J., and D. von Wettstein. 1992. Coordinator's report: Nuclear genes affecting the chloroplast. Stock list of mutants kept at the Carlsberg Laboratory. *Barley Genet. Newsl.* 21:102-108.
5. Tsuchiya, T. 1972. Allelism testing of various mutations in barley. *Barley Genet. Newsl.* 2:80-87.

Prepared:

T.E. Haus and T. Tsuchiya. 1971. *Barley Genet. Newsl.* 1:146

Revised:

T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:120.
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:206.
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:113.

BGS 202, Third outer glume 1, *trd1*

Stock number: BGS 202
Locus name: Third outer glume 1
Locus symbol: *trd1*

Previous nomenclature and gene symbolization:

Third glume = *t* (3).
Bracteate (6).
Bracteatum-c = *bra-c* (1).

Inheritance:

Monofactorial recessive (3, 4, 6, 7).
Located in chromosome 1HL (3, 4, 7); about 16.0 cM distal from the *Blp1* (black lemma and pericarp 1) locus (3, 4, 7); about 11.4 cM proximal from the *eam8* (early maturity 8) locus (8).

Description:

The characteristic trait of this mutant is the presence of a bract, third outer glume, outside the two empty glumes of the central spikelet. The bract associated with the lowest spikelet is always the largest, embracing in some cases about one-half the spike, and the bracts become progressively smaller toward the tip of the spike (7). Basal rachis internodes may be elongated. Although allelism tests were not conducted for the first three *trd* mutants, similar linkage values between the *trd* and *Blp* loci are reported (3, 4, 7). Takahashi et al. (7) assume that they used the same material studied by Miyake and Imai (6).

Origin of mutant:

A spontaneous mutant in *Hordeum vulgare* var *afghanicum* (3).

Mutational events:

trd1.a in *Hordeum vulgare* var. *afghanicum* (3, 6); *trd1.b* (GSHO 227) in Valki (CIho 5478) (4); *trd1.c* in a Japanese cultivar (6, 7); *trd1.d* (Mut 1969/61) in Proctor (PI 280420) (2); *bra-c.1* (,NGB 114303, GSHO 1695) in Bonus (PI 189763) (1); *bra-c.2* (NGB 114304), -c.3 (NGB 114305), -c.4 (NGB 114306), -c.5 (NGB 114307) in Bonus, -c.6 (NGB 114308, NGB 114309) in Foma (CIho 11333), -c.8 (NGB 114311, NGB 114312, NGB 114313) in Kristina (NGB 1500) (5).

Mutant used for description and seed stocks:

trd1.b (GSHO 227) in Valki; *bra-c.1* (GSHO 1695, NGB 114303) in Bonus; *trd1.b* from R.I. Wolfe's Chromosome 5 Marker Stock in Bowman (PI 483237)*7 (GSHO 2060); *trd1.b* in Bowman*8 (BW880, NGB 22314); *bra-c.1* in Bowman*4 (GSHO 2061); *bra-c.1* in Bowman*5 (BW069, NGB 20475).

References:

1. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
2. Häuser, H., and G. Fischbeck. 1972. Translocations and genetic analysis of other mutants. *Barley Genet. Newsl.* 2:28-29.
3. Ivanova, K.V. 1937. A new character in barley "third outer glume" — Its inheritance and linkage with color of the flowering glumes. *Bull. Appl. Bot., Genet., & Pl. Breed.* II. 7:339-353.
4. Konzak, C.F. 1953. The third outer glume character in barley. *J. Hered.* 44:103-104.
5. Lundqvist, U. (Unpublished).
6. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] *Bot. Mag., Tokyo* 36:25-38. [In Japanese.]
7. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage

studies in barley. Ber. Ohara Inst. landw. Forsch. 10:29-52.

8. Takahashi, R., and S. Yasuda. 1971. Genetics of earliness and growth habit in barley. p. 388-408. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:147.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:121.

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:207-208.

BGS 203, Black lemma and pericarp 1, *Blp1*

Stock number: BGS 203
Locus name: Black lemma and pericarp 1
Locus symbol: *Blp1*

Previous nomenclature and gene symbolization:

Black lemma and caryopsis = *B* (8).
Black pericarp = *Bk* (1).
Black lemma and pericarp = *B* (9).

Inheritance:

Monofactorial dominant (1, 6, 8).
Located in chromosome 1HL [5L] (5, 7); about 16.0 cM proximal from the *trd1* (third outer glume 1) locus (5); in 1H bin 13 about 8.8 cM proximal from RFLP marker ABC261 (2); associated with SNP markers 2_0959 to 2_0603 (positions 173.49 to 199.04 cM) in 1HL of the Bowman backcross-derived line BW062 and SNP marker 2_0940 (about position 179 cM) in 1HL of the Bowman backcross-derived line BW060 (3), in 1H bin 13.

Description:

Black pigmentation of the lemma and pericarp develops slightly before maturation of the spike. Pigmented organs may include all parts of the spike, awns, the upper portion of the stem, and upper leaves. The intensity of pigmentation associated with each of the dominant alleles at the *Blp1* locus is characteristic of that allele, and is relatively stable over environments (9). Black seed is produced by melanin-like pigment in the pericarp (1). Woodward (9) reports that the dominance ranking of alleles at the *Blp1* locus is related to the intensity of black pigmentation they confer, with the *Blp1.b* (*B*) allele conferring extreme black pigmentation. The *Blp1.mb* (*B^{mb}*) allele is associated with medium black and a reduced distribution pattern; and the *Blp1.g* (*B^g*) allele is associated with light black or gray coloration (9, 10). In the Bowman backcross-derived lines for the *Blp1* locus, BW060 and BW062, the expression of other morphological traits appeared similar to those of Bowman (4).

Origin of mutant:

Natural occurrence in several cultivars (8, 9).

Mutational events:

Blp1.b (*B*) in *Hordeum distichon* var *nigrinudum* No 1 (NSL 3286, GSHO 988) (9); *Blp1.mb* (*B^{mb}*) in Clho 2970 (GSHO 226) (9); *Blp1.g* (*B^g*) in Blackhull (Clho 878, GSHO 199) and Black Smyrna (Clho 191, GSHO 222) (9).

Mutant used for description and seed stocks:

Blp1.b in *Hordeum distichon* var *nigrinudum* No 1 (GSHO 988); *Blp1.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 3450) in Bowman (PI 483237)*8 (GSHO 2054, BW062, NGB 20470); likely *Blp1.g* from a Composite Cross in Bowman *5 (BW060, NGB 20468).

References:

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8 Tschermak, E. von. 1901. Über Züchtung neuer Getreiderassen mittelst künstlicher Kreuzung. Kritisch-historische Betrachtungen. Zeitschrift für das landwirtschaftliche Versuchswesen Oesterreich 4:1029-1060.

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10. Woodward, R.W. 1942. Linkage relationships between the allelomorphic series, B, B^{mb}, B^g, and A₁a₁ factors in barley. J. Amer. Soc. Agron. 34:659-661.

Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:148.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:209.

J.D. Franckowiak. 2007: Barley Genet. Newsl. 37:245-246.

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:69-70.

BGS 207, Albino seedling 1, *abo1*

Stock number: BGS 207
Locus name: Albino seedling 1
Locus symbol: *abo1*

Previous nomenclature and gene symbolization:

White seedling $t = a_t$ (2).

Albino seedling $t = a_t$ (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 1HL (2); over 22.3 cM proximal from the *Blp1* (black lemma and pericarp 1) locus (2); over 36.7 cM proximal from the *Blp1* locus (4).

Description:

Seedlings are white in color and devoid of normal pigments (2). Plants with this phenotype die at the two or three leaf stage and are classified as albino mutants (3). The *abo1.a* gene must be maintained as a heterozygous stock. The albino seedling mutant (line B17) described by Daane (1) may be the same as the one studied by Robertson (2). Both are reported as originating as a selection from the cultivar Trebi made at the University of Minnesota. Although some phenotypic differences and different map positions are reported (1, 2), both authors may have studied the same mutant. The mutant studied by Daane is not present in barley collections; thus, allelism tests are not possible.

Origin of mutant:

A spontaneous mutant in Trebi (PI 537442), which was obtained from the University of Minnesota (2).

Mutational events:

abo1.a (Trebi I, GSHO 51) in Trebi (PI 537442) (2).

Mutant used for description and seed stocks:

abo1.a (GSHO 51) in Trebi.

References:

1. Daane, A. 1931. Linkage relations in barley. Minnesota Agric. Exp. Stn. Tech Bull. 78. 30 p.
2. Robertson, D.W. 1929. Linkage studies in barley. Genetics 14:1-36.
3. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.
4. Woodward, R.W. 1942. Linkage relationships between the allelomorphic series, B, B^{mb}, B^g, and A_ta_t factors in barley. J. Am. Soc. Agron. 34:659-661.

Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:152.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:210.

BGS 208, Fragile stem 2, *fst2*

Stock number: BGS 208
Locus name: Fragile stem 2
Locus symbol: *fst2*

Previous nomenclature and gene symbolization:

Fragile stem 2 = *fs2* (13).

Inheritance:

Monofactorial recessive (10, 13).

Located in chromosome 1HL (9, 11, 12); over 19.0 cM proximal from the *nec1* (necrotic leaf spot 1) locus (2); 1.9 cM distal from molecular markers *wg789d* and *bcd351b* in 1H bin 08 (1); *fst2.b* is associated with SNP markers 1_0259 to 2_0997 (positions 70.78 to 89.01 cM) in 1H bins 07 to 08 of the Bowman backcross-derived line BW374 (1), in 1H bin 08.

Description:

The brittle leaf and stem characteristics of *fst2* plants are similar to those of *fst1* plants (9). Leaves and stems are very fragile and easily broken when slightly bent (13). Young leaves generally wither in the afternoon in the greenhouse and in the field during the spring. Most of the leaf blade tips turn yellow prior to heading and gradual die back is observed (9). Plants are about one-half normal height when protected in the greenhouse, but in the field plants are weak and are easily damaged by wind. Culm internodes are often curved (3). For the semidwarf, brittle stem mutants, *fst2* alleles *fst2.b* and *fst2.e* in their original stocks, the maximum flexural load (Newtons) required to bend the midpoint of each internode was 2 to 3 times lower than the load causing bending in their parents (1, 7, 8). Heading was delayed about four days in the Bowman backcross-derived line BW374. Compared to Bowman, plants of the BW374 line were about 1/2 normal height. Spikes had 3 to 4 fewer kernels. Kernels were small and thin and 1/2 to 2/3 of normal weight. Grain yields are very low (3). The *fst2* mutants were shown to have reduced levels of crystalline cellulose in their culms compared with their parental lines (6, 8). A custom-designed microarray used by Burton et al. (1) revealed a marked decrease in transcript levels of mRNA for the *HvCesA4* cellulose synthase gene. Sequencing of the *HvCesA4* gene of *fst2* mutants revealed the presence of a 964-bp solo long terminal repeat of a Copia-like retroelement in the first intron, which interferes with transcription or processing of the mRNA from the of the *HvCesA4* gene (1).

Origin of mutant:

A spontaneous mutant in Oshichi (OUJ755, PI 190273) (9, 10, 13).

Mutational events:

fst2.b (Oshichi-hen, OUL006, OUX054, GSHO 578) in Oshichi (OUJ755, PI 190273) (9, 10, 13); *fst2.e* (OUM245) in Shiroseto (OUJ156) (8).

Mutant used for description and seed stocks:

fst2.b (GSHO 578, OUX054) in Oshichi; *fst2.b* in Bowman (PI 483237)*7 (GSHO 2046); *fst2.b* in Bowman*8 (BW374, NGB 20613).

References:

1. Burton, R.A., G. Ma, U. Baumann, A.J. Harvey, N.J. Shirley, J. Taylor, F. Pettolino, A. Bacic, M. Beatty, C.R. Simmons, K.S. Dhugga, J.A. Rafalski, S.V. Tingey, and G.B. Fincher. 2010. A customized gene expression microarray reveals that the brittle stem phenotype *fs2* of barley is attributable to a retroelement in the *HvCesA4* Cellulose Synthase Gene 1. *Plant Physiol.* 153:1716-1728.

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10. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. *Ber. Ohara Inst. landw. Forsch.* 10:29-52.
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Prepared:

T.E. Haus and T. Tsuchiya. 1971. *Barley Genet. Newsl.* 1:153.

Revised:

R. Takahashi. 1972. *Barley Genet. Newsl.* 2:192.

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:211.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:114-115.

BGS 213, Spring growth habit 3, *Sgh3*

Stock number: BGS 213
Locus name: Spring growth habit 3
Locus symbol: *Sgh3*

Previous nomenclature and gene symbolization:

Spring habit of growth 3 = *Sh3* (3).

Inheritance:

Monofactorial dominant (3).

Located in chromosome 1HL (2, 4); over 35.8 cM proximal from the *Blp1* (black lemma and pericarp 1) locus (1, 2).

Description:

Cultivars with the *Sgh3.c* allele exhibit a highly spring habit (grade I) and plants form ear primordia under long-day conditions without prior cold treatment (2, 3). When near-isogenic lines for growth habit are grown at Kurashiki, Japan, the *Sgh3.c* allele has major influence on maturity and phenotype in the absence or presence of other spring habit of growth genes. Plants are 10 days or more earlier, tillers per plant are 30% less or more, kernel number is reduced by about 20%, and spike length is reduced (5).

Spring cultivars having only the *Sgh3.c* gene have never been found. Spring cultivars with the *Sgh2.1 Sgh3.c* genotype occur most frequently in North Pakistan, North India, Tibet, Ethiopia, and Northern Europe (6). The *Sgh3.c* allele is always accompanied by the *Sgh2.1* or the *sgh1.a* and *Sgh2.1* genes in cultivars (1, 2).

Origin of mutant:

Natural occurrence in many cultivars (2, 6).

Mutational events:

Sgh3.c occurs in many spring cultivars distributed mostly in regions of extremely high latitude or high altitude (2).

Mutant used for description and seed stocks:

Sgh3.c in a selection from the cross Tammi X Hayakiso 2 (GSHO 764), which has the winter habit alleles at the *sgh1* and *Sgh2* loci (2).

References:

1. Takahashi, R., and S. Yasuda. 1956. Genetic studies of spring and winter habit of growth habit in barley. Ber. Ohara Inst. landw. Biol., Okayama Univ. 10:245-308.
2. Takahashi, R., and S. Yasuda. 1971. Genetics of earliness and growth habit in barley. p. 388-408. In R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
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6. Yasuda, S., J. Hayashi, and I. Moriya. 1986. Genotype differentiation in spring growth habit of barley strains collected from northern parts of Pakistan and India. Barley Genet. Newsl. 16:18-19.

Prepared:

S. Yasuda. 1972. Barley Genet. Newsl. 2:191.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:212.

BGS 214, Early maturity 8, *eam8*

Stock number: BGS 214
Locus name: Early maturity 8
Locus symbol: *eam8*

Previous nomenclature and gene symbolization:

Early heading *k* = *ea_k* (27).
Early maturity-*a* = *ea-a* (9, 22).
Praematurum-*a* = *mat-a* (4, 9, 14, 15, 27).
Erectoides-*o* = *ert-o* (9, 19).
Hordeum vulgare Early flowering 3 = *HvElf3* (28).

Inheritance:

Monofactorial recessive (4, 8).
Located in chromosome 1HL (22); about 11.4 cM distal from the *trd1* (third outer glume 1) locus and 20.9 cM distal from the *Blp1* (black lemma and pericarp 1) locus (22, 25); *eam8.w* is associated with SNP markers 2_0603 to 2_0138 (positions 199.04 to 202.26 cM) in 1H in bin 14 of the Bowman backcross-derived line BW290 (3); *eam8.k* is associated with SNP markers 1_0782 to 1_0443 (positions 193.83 to 206.12) in 1H bin 14 of the Bowman backcross-derived line BW289 (3); *ert-o.16* is associated with SNP markers 1_0911 to 1_1509 (positions 177.51 to 199.04) in 1H bins 13 to 14 of the Bowman backcross-derived line BW319 (3), in 1H bin 14.

Description:

Early heading is associated with decreased culm length, spike length, kernels per spike, and grain yield (17, 25, 27). Mutant plants are day-length neutral or photoperiod insensitive when grown in the fall at Kurashiki, Japan (27). They head about 20 days earlier than the standard mid-season cultivar, Akashinriki. Day-length neutrality was observed in early heading mutants isolated from spring barley in Sweden (2, 10). Under controlled environmental conditions, number of days to heading did not change as photoperiod is altered (2, 11). All *mat-a* induced mutants were characterized by yellowish-green seedlings at an early stage of development under controlled environmental conditions (1). Other *eam8* mutants showed a similar response by becoming yellow green under specific growing conditions, 8 to 12 hours of illumination at low temperatures (below 10°C) plus high temperature (20°C or higher) during the dark period (6, 22, 25). The color change is caused by photothermal stress, which increases the zeaxanthin content at the expense of chlorophyll and other pigments (6, 20, 25). The mutant stock *mat-a.8* was released as the cultivar Mari (10, 12). When grown under 12 h days, the levels of phytochrome B (*phyB*) decreased in light-grown BMDR-1 plants, containing a mutant allele at the *eam8* locus, compared to normal plants (13). The instability of *phyB* content was reported to be responsible for photoperiod insensitivity of *eam8* mutants (13). Under continuous light and with far-red light treatment for seven days, most differences in heading date between BMDR-1 and BMDR-8 (Shabet) are eliminated (20). The *Mat-a* or *Eam8* (*HvElf3*) locus has been cloned and is a homolog of the *Arabidopsis thaliana* circadian clock regulator Early Flowering 3 (*Elf3*). Among 87 *mat-a* alleles identified >20 different *mat-a* alleles had mutations leading to the defective putative ELF3 protein (28). The effects *mat-a* mutants on the development of reproductive structures might be explained by pronounced expression of flowering inducing genes like *Gigantea* (*AtGI*) (28).

Origin of mutant:

An X-ray induced mutant in Maja (PI 184884, NGB 8815) (7, 8, 11); natural occurrence in Kinai 5 (OUJ493) and Kagoshima Gold (OUJ219) (22, 26).

Mutational events:

ert-o.16 (NGB 112618, GSHO 489) in Maja (PI 184884, NGB 8815) (7); *eam8.k* in Kagoshima Gold (OUJ 219), Kinai 5 (OUJ493, GSHO 765, Clho 11560), and Kindoku (OUU332) (22, 23, 26); *mat-a.8* (NGB 1491, NGB 4694, NGB 14656, NGB 110008), -*a.11* (NGB 110011), -*a.12* (NGB 110012) in Bonus (PI 189763) (8, 15); *mat-a.27* (NGB 110027), -*a.45* (NGB 110045), -*a.46* (NGB 110046), -*a.48* (NGB 110048), -*a.62* (NGB 110062) in Bonus, -*a.110* (NGB 110110), -*a.130* (NGB 110130), -*a.153* (NGB 110153), -*a.221* (NGB 110221), -*a.238* (NGB 110238), -*a.255* (NGB 110255), -*a.272* (NGB 110272), -*a.274* (NGB 110274), -*a.287* (NGB 110287), -*a.289* (NGB 110289), -*a.294* (NGB 110294), -*a.325* (NGB 110325), -*a.338* (NGB 110338), -*a.370* (NGB 110370), -*a.384* (NGB 110384), -*a.390* (NGB 110390), -*a.404* (NGB 110404), -*a.406* (NGB 110406), -*a.407* (NGB 110407) in Foma (Clho 11333), -*a.509* (NGB 110509), -*a.641* (NGB 110641), -*a.703* (NGB 110703), -*a.733* (NGB 110733), in Kristina (NGB 1500), -*a.753* (NGB 110753), -*a.796* (NGB 110796), -*a.797* (NGB 110797), -*a.813* (NGB 110813), -*a.832* (NGB 110832), -*a.903* (NGB 116858), -*a.909* (NGB 117440), -*a.921* (NGB 117452) in Bonus, -*a.961* (NGB 117492), -*a.970* (NGB 117501), -*a.976* (NGB 117507), -*a.984* (NGB 117515), -*a.1011* (NGB 117542), in Sv 79353, -*a.1032* (NGB 117563), -*a.1033* (NGB 117564), -*a.1034* (NGB 117565), -*a.1035* (NGB 117566), -*a.1036* (NGB 117567), -*a.1037* (NGB 117568), -*a.1039* (NGB 117570), -*a.1040* (NGB 117571), -*a.1041* (NGB 117572), -*a.1042* (NGB 117573), -*a.1043* (NGB 117574), -*a.1044* (NGB 117575), -*a.1045* (NGB 117576), -*a.1046* (NGB 117577), -*a.1047* (NGB 117578), -*a.1048* (NGB 117579), -*a.1049* (NGB 117580) in Sv Vg74233 (14); *mat-a.1050* (NGB 117581), -*a.1051* (NGB 117582), -*a.1052* (NGB 117583), -*a.1053* (NGB 117584), -*a.1054* (NGB 117585), -*a.1055* (NGB 117586), -*a.1056* (NGB 117587), -*a.1057* (NGB 117588), -*a.1058* (NGB 117589), -*a.1059* (NGB 117590), -*a.1060* (NGB 117591), -*a.1061* (NGB 117592), -*a.1062* (NGB 117593), -*a.1063* (NGB 117594), -*a.1064* (NGB 117595), -*a.1065* (NGB 117596), -*a.1067* (NGB 117598), -*a.1069* (NGB 117600), -*a.1070* (NGB 117601), -*a.1071* (NGB 117602), -*a.1072* (NGB 117603), -*a.1073* (NGB 117604), -*a.1074* (NGB 117605) in Sv Vg74233 (16); *eam8.q* (Ea8), *eam8.r* (Ea9), *eam8.s* (Ea10), *eam8.t* (Ea16) in Chikurin Ibaraki 1 (OUJ069, Clho 7370, GSHO 783) (24); *eam8.u* (Mut 2571) in Donaria (PI 161974) (6, 18); *eam8.v* in Munsing (Clho 6009, GSHO 636) (5, 20, 21); *eam8.w* in Early Russian (Clho 13839) (5), BMDR-1 (*eam8.y*) from the original mutant in a dwarf line backcrossed to Shabet (Clho 13827) (20).

Mutant used for description and seed stocks:

eam8.k in Kinai 5 (OUJ266, GSHO 765, Clho 11560); *ert-o.16* (GSHO 489, NGB 112618) in Maja; *eam8.k* from Kinai 5 in Bonus*5 (26); *mat-a.8* from Bonus in Tochigi Golden*5 (26); *eam8.v* from Munsing in Titan (Clho 16526)*7 (21); *eam8.k* in Bowman (PI 483237)*7 (GSHO 2063, BW289, NGB 20573); *eam8.w* from Early Russian in Bowman*7 (BW290, NGB 20574); *ert-o.16* from Maja in Bowman*7 (GSHO 2064); *ert-o.16* in Bowman*8 (BW319, NGB 22114).

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www.pnas.org.lookup/suppl/doi:10.1073/pnas.111309109.

Prepared:

S. Yasuda. 1972. *Barley Genet. Newsl.* 2:198.

Revised:

J.D. Franckowiak, U. Lundqvist, T. Konishi, and L.W. Gallagher. 1997. *Barley Genet. Newsl.* 26:213-215.

J.D. Franckowiak and U. Lundqvist. 2007. *Barley Genet. Newsl.* 37:247-250.

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:116-119.

BGS 215, Desynapsis 6, *des6*

Stock number: BGS 215
Locus name: Desynapsis 6
Locus symbol: *des6*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 1H (1).

Description:
The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is 7.9 ± 2.1 ranging from 7 ring bivalents ($d = 0$) to 14 univalents ($d = 14$). Many univalents split longitudinally during anaphase I. Lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore quartets contain an average of 3.3 micronuclei per quartet with a range of 0 to 12. Ovule fertility is about 16%, and about 22% of the selfed seeds are trisomics (1).

Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (3, 4).

Mutational events:
des6.i (GSHO 597) in Betzes (PI 129430) (3, 4); *des6.m* in OAC 21 (CIho 1740), *des6.o* in Betzes (2, 4).

Mutant used for description and seed stocks:
des6.i (GSHO 597) in Betzes; *des6.i* in Bowman (PI 483237)*6 (BW244, NGB 22070); *des6.o* in Bowman*5 (BW245, NGB 22071).

References:
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Prepared:
J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:129.

Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:216.

BGS 218, Reaction to *Puccinia hordei* 4, *Rph4*

Stock number: BGS 218
Locus name: Reaction to *Puccinia hordei* 4 (barley leaf rust)
Locus symbol: *Rph4*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* D = D (7).
Resistance to *Puccinia hordei* Otth 4 = Pa₄ (8).

Inheritance:

Monofactorial dominant (5, 7).
Located in chromosome 1HS (4, 5); about 16.0 cM distal from the *Reg1* (reaction to *Erysiphe graminis* 1) or *Mla* locus (3, 4); associated with SNP marker 2_0479 (position 0.0 cM) in 1HS of the Bowman backcross-derived line BW753, and SNP markers 2_0479 to 1_0654 (positions 0.0 to about 2 cM) in 1HS of the Bowman line BW752) (1), in 1H bin 01.

Description:

The seedling reaction type is 0;ⁿ - 1^c with race 4 culture 57-19. Heterozygotes may have a type 2 or 3 reaction under certain conditions (8). Very few *P. hordei* isolates produce a resistant reaction to the *Rph4* gene even though the gene is present in a number of cultivars (2).

Origin of mutant:

Natural occurrence in Gull (Gold) (Clho 1145, GSHO 466, NGB 1480) and Lechtaler (Clho 11519) (5, 6).

Mutational events:

Rph4.d in Gull (GSHO 1314) and Lechtaler (5, 6); *Rph4.d* in Franger (Clho 8811) (9).

Mutant used for description and seed stocks:

Rph4.d in Gull (GSHO 1314); *Rph4.d* from Gull in Bowman (PI 483237)*2 (GSHO 2322); *Rph4.d* from Gull in Bowman*6 (BW752, PI 643153, NGB 22458); *Rph4.d* from Lechtaler in Bowman*6 (GSHO 3419, BW753, NGB 20459).

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Prepared:

C.W. Roane. 1976. *Barley Genet. Newsl.* 6:129.

Revised:

J.D. Franckowiak and Y. Jin. 1997. *Barley Genet. Newsl.* 26:217.

J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:302-303.

BGS 220, Chlorina seedling 3, *fch3*

Stock number: BGS 220
Locus name: Chlorina seedling 3
Locus symbol: *fch3*

Previous nomenclature and gene symbolization:

Chlorina seedling 3 = *f3* (3).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 1HS (4, 5, 6, 7); near the tip of 1HS associated with SNP markers 2_0479 to 3_0969 (at position 0.0 cM) in 1HS of the Bowman backcross-derived line BW359 (1), in 1H bin 01.

Description:

Seedlings have bright yellow leaves, which gradually change color to a light green as the plant grows. Plants are vigorous, but remain chlorina or light green until maturity. Plants expressing the *fch3.d* gene can be distinguished readily from normal plants at all stages of growth (3, 4). Heading of plants in the Bowman backcross-derived line BW359 was delayed by 5 to 8 days, plants were about 3/4 of normal height, seeds were 10 to 20% lighter, and seed yields were less than 1/2 of normal (2).

Origin of mutant:

A spontaneous mutant in an unknown six-rowed cultivar (3).

Mutational events:

fch3.d (Minn 89-4, GSHO 851) in an unknown cultivar (3).

Mutant used for description and seed stocks:

fch3.d (GSHO 851) in an unknown cultivar; *fch3.d* in Bowman (PI 483237)*6 (GSHO 2033); *fch3.d* in Bowman*7 (BW359, NGB20598).

References:

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Prepared:

A. Shahla and T. Tsuchiya. 1979. *Barley Genet. Newsl.* 9:132.

Revised:

J.D. Franckowiak and A. Hang. 1997. *Barley Genet. Newsl.* 26:218.
J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:71.

BGS 221, White streak 5, *wst5*

Stock number: BGS 221
Locus name: White streak 5
Locus symbol: *wst5*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Located in chromosome 1HL (3); about 34.5 cM distal from the *nec1* (necrotic leaf spot 1) locus (1, 2, 3); about 21.7 cM proximal from the *Blp1* (black lemma and pericarp 1) locus (1, 2, 4).

Description:
White streaks with poorly defined margins may develop on the foliage, but expression is influenced by environment and possibly genetic background. Some environmental conditions cause the plants to be nearly albinotic from the seedling stage until heading when the plants turn green; while under other conditions the streaks seem absent (4).

Origin of mutant:
A mutant induced by combined treatment with gamma-rays and diethyl sulfate of Carlsberg II (CIho 10114, NGB 5085) (4).

Mutational events:
wst5.e (Mutant no 10, GSHO 591) in Carlsberg II (CIho 10114, NGB 5085) (3).

Mutant used for description and seed stocks:
wst5.e (GSHO 591) in Carlsberg II.

References:
1. Jensen, J. 1978. Location of the *eceriferum* locus *cer-zi* on barley chromosome 5. Barley Genet. Newsl. 8:59-60.
2. Jensen, J. 1992. Coordinator's report: Chromosome 5. Barley Genet. Newsl. 21:89-92.
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Prepared:
J. Jensen. 1981. Barley Genet. Newsl. 11:100.

Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:219.

BGS 222, Necrotic leaf spot 1, *nec1*

Stock number: BGS 222
Locus name: Necrotic leaf spot 1
Locus symbol: *nec1*

Previous nomenclature and gene symbolization:

Mutant no. 10 (2).
Parkland spot = *sp.,b* (1).

Inheritance:

Monofactorial recessive (2, 4).
Located in chromosome 1HL (1, 2, 4); near the centromere (1), about 34.5 cM proximal from the *wst5* (white streak 5) locus (3, 5); about 10.0 cM distal from the *msg1* (male sterile genetic 1) locus (4, 6); near EST marker BF630384 in 5H bin 09 (7).

Description:

Small black-brown spots develop on all light-exposed parts of the plant starting near the leaf tip at the three-leaf stage (1, 2). The spots are oval (the longest dimension is parallel to the leaf veins) and generally less than 1 to 2 mm in size. The spots are concentrated in awn and the most distal parts of the leaf blade, but may occur on all plant parts (2, 4). The *nec1* locus is an orthologue of *Arabidopsis* necrotic mutant *HLM1* that encodes the cyclic nucleotide-gated ion channel 4 (7).

Origin of mutant:

A mutant induced by combined treatment with gamma-rays and diethyl sulfate of Carlsberg II (CIho 10114, NGB 5085) (2).

Mutational events:

nec1.a (Mutant no 10, GSHO 989) in Carlsberg II (CIho 10114, NGB 5085) (2, 3); *nec1.c* (*sp.,b*, GSHO 1284) in Parkland (CIho 10001) (1, 4); a mutant in Morex (CIho 15773) (6); FN085 and FN370 in Steptoe (CIho 15229) (7); *nec1.i* (FN338) in Morex (CIho 15773) (7).

Mutant used for description and seed stocks:

nec1.a (GSHO 989) in Carlsberg II; *nec1.c* from R.I. Wolfe's Multiple Marker Stock for Chromosome 5 in Bowman (PI 483237)*7 (GSHO 2052, BW628, NGB 22194); *nec1.i* in Bowman*2 (BW627, NGB 22193).

References:

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Genomics 275:159-168.

Prepared:

J. Jensen. 1981. Barley Genet. Newsl. 11:101.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:220.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:251-252.

BGS 223, Zebra stripe 3, *Zeb3*

Stock number: BGS 223
Locus name: Zebra stripe 3
Locus symbol: *Zeb3*

Previous nomenclature and gene symbolization:

Zoned leaf c = *zb_c* (2, 4, 5, 6, 9).
Zebra stripe c = *zb_c* (6, 7).
Zoned leaf c2 = *zb_c2* (2, 4, 5).
Zebra stripe c2 = *zb_c2* (6).
Zebra stripe 3 = *zb3* (7).

Inheritance:

Monofactorial incomplete dominant (2, 8, 9).
Located in chromosome 1HL (2, 4); associated with SNP markers 1_0275 to 2_0997 (positions 63.72 to 89.01 cM) in 1H of a heterozygous plant from the Bowman backcross-derived line BW932 (1), in 1H bin 08.

Description:

Early leaves of homozygous plants have bright yellow bands across a light yellow background when grown under alternating temperatures, warm day and cool night (2). Later leaves have patches of bright yellow. Cool temperatures enhance the yellow banding while warm temperatures increase green pigments. Under very cold conditions, leaves become yellowish white and deteriorate. Heterozygotes have slightly pale green color compared to normal plants (2). The *Zeb3.c* gene must be maintained as a heterozygous stock because seed production on mutant plants is rare.

Origin of mutant:

A spontaneous mutant from the collection of genetic stocks maintained by Woodward (2, 5).

Mutational events:

Zeb3.c (Utah 41, Alb Acc 43, GSHO 1451) in an unknown cultivar (2, 3, 5).

Mutant used for description and seed stocks:

Zeb3.c (GSHO 1451) in an unknown cultivar; *Zeb3.c* in Bowman (PI 483237)*3 (GSHO 2057); *Zeb3.c* in Bowman*7 (BW932, NGB 22361).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
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6. Tsuchiya, T. 1983. Proposed new gene symbol for two different mutant types for zebra Colorado, or zoned leaf. *Barley Genet. Newsl.* 13:84.
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9. Woodward, R.W. 1957. Linkages in barley. Agron. J. 49:28-32.

Prepared:

T. Tsuchiya and A. Shahla. 1984. Barley Genet. Newsl. 14:94 as BGS 223, Zoned leaf 3 or zebra striped leaf 3.

Revised:

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:221.

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:72-73.

BGS 224, Erectoides-b, *ert-b*

Stock number: BGS 224
Locus name: Erectoides-b
Locus symbol: *ert-b*

Previous nomenclature and gene symbolization:

Erectoides-2 = *ert-2* (3, 5).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 1HL (9, 10, 11, 12, 13); slightly distal from the *cer-e* (eceriferum-e) locus (6, 13, 14); and about 19.3 cM proximal from the *nec1* (necrotic leaf spot 1) locus (7); associated with SNP markers 1_0259 to 1_0520 (positions 70.78 to 82.35 cM) in 1HL of the Bowman backcross-derived line BW304 (1), likely in 1H bin 08.

Description:

Spikes have a compact appearance caused by a reduction in rachis internode length with rachis internode length values from 1.9 to 2.3 mm. Culms are shorter than those of parental cultivars (12). GA₃ treatment of plants as the flag leaf emerges decreased spike density (15). Plants of the Bowman backcross-derived line had slightly shortened peduncles and were about 5/6 of normal height. Rachis internode lengths were 3.5 vs. 4.4 mm. Kernels were slightly shorter and wider and weights were often about 10% higher. Grain yields were about 3/4 of normal (2).

Origin of mutant:

An X-ray induced mutant in Gull (CIho 1145, GSHO 466) (3, 4, 5).

Mutational events:

ert-b.2 (NGB 112606, GSHO 470), *-b.4* (NGB 112607), *-b.5* (NGB 112608), *-b.9* (NGB 112611) in Gull (CIho 1145, GSHO 466) (4); *ert-b.128* (NGB 112727), *-b.151* (NGB 112750) in Bonus (PI 189763) (12); *ert-b.174* (NGB 112775) in Bonus, *-b.333* (NGB 112848) in Foma (CIho 11333) (8); *ert-b.354* (NGB 112870), *-b.394* (NGB 112911) in Foma (12).

Mutant used for description and seed stocks:

ert-b.2 (GSHO 470, NGB 112606) in Gull; *ert-b.2* in Bowman (PI 483237)*7 (GSHO 2049, BW304, NGB 20586).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å. 1947. Mutations in agricultural plants. Hereditas 33:1-100.
4. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
5. Hagberg, A., N. Nybom, and Å. Gustafsson. 1952. Allelism of *erectoides* mutations in barley. Hereditas 38:510-512.
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7. Jensen, J. 1981. Location of the high-lysine locus *Lys4d* on barley chromosome 5. Barley Genet. Newsl. 11:45-47.
8. Lundqvist, U. (Unpublished).
9. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. Hereditas 62:25-96.

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11. Persson, G., and A. Hagberg. 1965. Localization of nine induced mutations in the barley chromosomes. *Barley Newsl.* 8:52-54.
12. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.
13. Søgaaard, B. 1971. Linkage studies on eceriferum mutants in barley. *Barley Genet. Newsl.* 1:41-47.
14. Søgaaard, B. 1973. Continued linkage studies on eceriferum mutants in barley. *Barley Genet. Newsl.* 3:57-61.
15. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. *Hereditas* 58:359-384.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:222.

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:74-75.

BGS 225, Curled leaf dwarf 1, *clh1*

Stock number: BGS 225
Locus name: Curled leaf dwarf 1
Locus symbol: *clh1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Located in chromosome 1HL (3, 4); about 7.0 cM from the *msg1* (male sterile genetic 1) locus (4); located in chromosome 7HL or 5HL based on SNP markers retained in Bowman backcross-derived line BW182, SNP markers 1_1243 to 2_0365 (positions 167.56 to 229.66 cM) in 7HL and SNP markers 1_1456 to 2_1177 (positions 195.82 to 203.85 cM) in 5HL (2).

Description:
Leaf blades are erect, narrow and folded inward and appear thicker than normal. Plants show reduced vigor, fertility, and height (3/4 of normal) when grown in the greenhouse; further reduction in vigor and fertility is observed when mutants are grown in the field. Spikes emerge poorly from the boot (2). Plants of the Bowman backcross-derived line BW182 were 30 to 40% shorter than Bowman. Kernels were slightly thinner and were about 2/3 normal weight. Plants produced very little grain (2).

Origin of mutant:
A neutron induced mutant in Hannchen (PI 10585) (4).

Mutational events:
clh1.a (GSHO 1212) in Hannchen (PI 10585) (4).

Mutant used for description and seed stocks:
clh1.a (GSHO 1212) in Hannchen; *clh1.a* in Bowman (PI 483237)*2 (GSHO 2051);
clh1.a in Bowman*5 (BW182, NGB 22014).

References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
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Prepared:
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:223.

Revised:
J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:76.

BGS 226, Revoluted leaf 1, *rvl1*

Stock number: BGS 226
Locus name: Revoluted leaf 1
Locus symbol: *rvl1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (2).
Located in chromosome 1HL (2, 4); proximal from the *trd1* (third outer glume 1) locus, and distal from the *abo1* (albino seedling 1) locus (2), associated with SNP markers 1_0764 to 1_1006 (positions 61.55 to 110.10 cM) in 1H bins 08 to 10 of the Bowman backcrossed-derived line BW763 (1).

Description:
Tips of young leaf blades tend to roll into a tube through a counter-clockwise spiral, compared to flat surfaces of the control. Segregates can be scored from the three-leaf stage until near maturity (2). Mutant plants of the Bowman backcross-derived line BW763 were 75 to 90% of normal height and peduncle length varied from slightly reduced to 2/3 of normal. Kernel weights were slightly lower and grain yields approached normal (3).

Origin of mutant:
An X-ray induced mutant in Hakata 2 (OUJ807, PI 263407) (2).

Mutational events:
rvl1.a (Kmut 103, GSHO 608) in Hakata 2 (OUJ807, PI 263407) (2, 4).

Mutant used for description and seed stocks:
rvl1.a (GSHO 608) in Hakata 2; *rvl1.a* from Hakata 2 in Bowman (PI 483237)*1 (GSHO 2319); *rvl1.a* in Bowman*5 (BW763, NGB 22231).

References:
1 Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic Dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
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Prepared:
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:224.

Revised:
J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:77.

BGS 227, Small lateral spikelet 1, *s/s1*

Stock number: BGS 227
Locus name: Small lateral spikelet 1
Locus symbol: *s/s1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Located in chromosome 1HL (3); closely linked to the *msg1* (male sterile genetic 1) locus (3); associated with SNP markers 1_0933 to 3_0343 (positions 82.35 to 87.19 cM) in 1HL) of the Bowman backcross-derived line BW867 (1), in 1H bin 08.

Description:
Sterile lateral spikelets become progressively smaller toward the tip of two-rowed spikes in plants, which express the *Vrs1.b* and *int-c.b* alleles at the six-rowed spike 1 and intermedium spike-c loci, respectively. The terminal rachis nodes generally have rudimentary lateral spikelets. Expression of the *s/s1* is affected by genetic background, but express is stronger often in late tillers. The trait can be observed only in some two-rowed segregates from crosses between six- and two-rowed cultivars. No significant differences in agronomic traits were observed between backcross-derived BW867 and Bowman, but kernels tended to be wider and heavier and test weights are slightly higher (2).

Origin of mutant:
Natural occurrence in six-rowed cultivars derived from Manchurian introductions, but it cannot be observed visually in six-rowed barley cultivars.

Mutational events:
s/s1.a in MSS005 [*msg1.ca* from Clho 5368 in Betzes (PI 129430)*11 (GSHO 1810)];
s/s1.a in Morex (Clho 15773, GSHO 2492).

Mutant used for description and seed stocks:
s/s1.a in Morex (GSHO 2492); *s/s1.a* from MSS005 in Bowman (PI 483237)*8 (GSHO 2034, BW867, NGB 22304).

References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.

Prepared:
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:225.

Revised:
J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:78.

BGS 228, Subcrown internode length 1, *Sil1*

Stock number: BGS 228
Locus name: Subcrown internode length 1
Locus symbol: *Sil1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial incomplete dominant (1).
Located in chromosome 1H (4); based on linkage drag with the *s/s1* (small lateral spikelet 1) locus (4); associated with SNP markers 1_0259 to 1_0890 (positions 70.78 to 110.10 cM) in the 1H centromeric region of the Bowman backcross-derived line BW852 (2), likely in 1H bin 08 or 09.

Description:
Plants have relatively short subcrown internodes, 0.0 to 1.0 cm, when planted 9 cm deep in vermiculite. Planting depth and subcrown internode length determine the position of the crown in relation to the soil surface (1). Plants with a deeper crown placement show higher levels of winter survival (5). In generating the Bowman backcross-derived line, the *Sil1* gene showed a dominant inheritance pattern. No other morphological effects for the *Sil1.a* gene were noted in Bowman backcross-derived line BW852 (3).

Origin of mutant:
Natural occurrence in NE 62203 (CIho 15542), a selection of unknown origin (1).

Mutational events:
Sil1.a in winter barley NE 62203 (1) (CIho 15542 GSHO 1604).

Mutant used for description and seed stocks:
Sil1.a in NE 62203 (GSHO 1604); *Sil1.a* in Bowman (PI 483237)*5 (GSHO 2032); *Sil1.a* in Bowman*7 (BW852, NGB 22289).

References:
1. Dofing, S.M., and J.W. Schmidt. 1984. Inheritance of subcrown internode length in a winter barley cross. *Crop Sci.* 24:692-694.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
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Prepared:
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:226.

Revised:
J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:79.

BGS 229, Curly dwarf 2, *cud2*

Stock number: BGS 229
Locus name: Curly dwarf 2
Locus symbol: *cud2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Located in chromosome 1HL (1); about 14.6 cM proximal from the *Blp1* (black lemma and pericarp 1) locus (1, 2).

Description:

Lemmas and awns are curly or strongly twisted, and stem internodes are curved. Culms are short (1/2 normal), spikes are semi-compact, awns are short (2/3 normal length), and kernels are globe-shaped. Most leaves are short and slightly twisted (1).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (1).

Mutational events:

cud2.b (OUM112, GSHO 1712) in Akashinriki (OUJ659, PI 467400) (1).

Mutant used for description and seed stocks:

cud2.b (GSHO 1712) in Akashinriki; *cud2.b* in Bowman (PI 483237)*2 (GSHO 2062); *cud2.b* in Bowman*7 (BW199, NGB 22031).

References:

1. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley VI. Ten mutant genes located on chromosomes 1 to 7, except 3. Ber. Ohara Inst. landw. Biol., Okayama Univ. 18:227-250.
2. Jensen, J. 1986. Coordinator's report: Chromosome 5. Barley Genet. Newsl. 16:32-34.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:227.

BGS 230, Globosum-e, *glo-e*

Stock number: BGS 230
Locus name: Globosum-e
Locus symbol: *glo-e*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Located in chromosome 1HL (1).

Description:

Plants appear normal, but kernels are larger and more rounded than those of normal sibs.

Origin of mutant:

A neutron induced mutant in Foma (Clho 11333) (2).

Mutational events:

glo-e.15 (*glo-e.1010*, NGB 115633, GSHO 1755) in Foma (Clho 11333) (1, 2).

Mutant used for description and seed stocks:

glo-e.15 (NGB 115633, GSHO 1755) in Foma; *glo-e.15* in Bowman (PI 483237)*7 (GSHO 2050, BW396, NGB 20634).

References:

1. Häuser, H., and G. Fischbeck. 1980. Genetic analysis of induced mutations. Barley Genet. Newsl. 10:30-31.
2. Lundqvist, U. (Unpublished).

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:228.

BGS 231, Curly 5, *cur5*

Stock number: BGS 231
Locus name: Curly 5
Locus symbol: *cur5*

Previous nomenclature and gene symbolization:

Curly 5 = *cu5* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 2HS (1); *cur5.h* is associated with SNP markers 1_1078 to 2_0476 (positions 66.78 to 96.47 cM) in 2HL bins 05 to 07 of the Bowman backcross-derived line BW225 (1); *cur5.h* is associated with SNP markers 1_0498 to 2_0476 (positions 81.43 to 96.47 cM) in 2HL bin 07 of the Bowman backcross-derived line BW250, which also contains dusky 1 (*dsk1.a*) (1). Previously located in chromosome 1HS (4); based on linkage drag with the *sls1* (small lateral spikelet 1) locus (4).

Description:

Leaves are short and partially coiled, and awns are slightly coiled. Plants are semidwarf (2/3 normal height), have relatively short spikes, and are relatively weak (2, 3). Plants of the Bowman backcross-derived line for *cur5.h*, BW225, headed 3 days later than Bowman and were about half as tall. Leaf blades of BW225 were short and narrow compared to those of Bowman. Spikes contain 5 fewer kernels, kernel were narrower (3.3 vs. 3.7 mm), and kernel weights were 10 to 15% lower. (3).

Origin of mutant:

A sodium azide induced mutant in Glenn (CIho 15769) (2).

Mutational events:

cur5.h (GSHO 1710) in Glenn (CIho 15769) (2, 3).

Mutant used for description and seed stocks:

cur5.h (GSHO 1710) in Glenn; *cur5.h* in Bowman (PI 483237)*8 (BW225, NGB 22052); *cur5.h* with *dsk1.a* in Bowman*7 (GSHO 2045, BW250, NGB 22075).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Faue, A.C. 1987. Chemical mutagenesis as a breeding tool for barley. M.S. Thesis. North Dakota State Univ., Fargo.
3. Franckowiak, J.D. (Unpublished).
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5. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.

Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:229.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:120.

BGS 232, High lysine 4, *Lys4*

Stock number: BGS 232
Locus name: High lysine 4
Locus symbol: *Lys4*

Previous nomenclature and gene symbolization:

Shrunken endosperm xenia 5 = *sex5g* (8).

Inheritance:

Monofactorial incomplete dominant (1, 5).

Located in chromosome 1HS (5, 6, 8); over 35.1 cM distal from the *ert-b* (erectoides-b) locus (6); associated with SNP markers 2_0373 to 1_0744 (positions 0.0 to 39.84 cM) in 1H bins 01 to 03 of the Bowman backcross-derived line BW497 (3).

Description:

At the hard dough stage, kernels homozygous for the *Lys4.d* gene develop a depression near the center of the lemma, which becomes progressively more distinct as the kernels mature. Grain produced by mutant plants has a 9% increase in lysine content (1, 2). Shrunken endosperm has a pleiotropic association with the high lysine gene *Lys4.d* (5). Kernels heterozygous at the *Lys4* locus may develop a slightly less distinct depression on the dorsal side (5). Maintenance of *Lys4.d* stocks may be difficult because outcrosses are not recognized easily. Plants of Bowman backcross-derived line BW497 were slightly shorter and kernel weights and grain yields were about 2/3 of normal (4).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bomi (PI 43371) (2).

Mutational events:

Lys4.d (Risø 8, GSHO 2475) in Bomi (PI 43371) (1, 2, 7).

Mutant used for description and seed stocks:

Lys4.d (GSHO 2475) in Bomi; *Lys4.d* in Bowman (PI 483237)*5 (GSHO 2035, BW497, NGB 20725).

References:

1. Doll, H. 1976. Genetic studies of high lysine barley mutants. p. 542-546. *In* H. Gaul (ed.) Barley Genetics III. Proc. Third Int. Barley Genet. Symp., Garching, 1975. Verlag Karl Thieme, München.
2. Doll, H., B. Kjøie, and P.O. Eggum. 1974. Induced high-lysine mutants in barley. *Radiat. Bot.* 14:73-80.
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4. Franckowiak, J.D. (Unpublished).
5. Jensen, J. 1979. Chromosomal location of one dominant and four recessive high-lysine genes in barley mutants. Vol. 1. p. 89-96. *In* Seed Protein Improvement in Cereals and Grain Legumes. Proc. Int. Symp., Neuherberg, Germany, 1978. Int. Atomic Energy Agency, Vienna.
6. Jensen, J. 1981. Location of the high-lysine locus *Lys4d* on barley chromosome 5. *Barley Genet. Newsl.* 11:45-47.
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Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:230.
Revised:
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:80-81.

BGS 233, Xantha seedling 7, *xnt7*

Stock number: BGS 233
Locus name: Xantha seedling 7
Locus symbol: *xnt7*

Previous nomenclature and gene symbolization:

Xantha seedling 66 = x_{66} (1).
Albino seedling a = *alb*,a (1).
Xantha seedling g = *xan*,g (2).

Inheritance:

Monofactorial recessive (1, 2).
Located in chromosome 1HL (2); about 2.0 cM from the *msg1* (male sterile genetic 1) locus (2).

Description:

Seedlings have a yellow color and die at the two to three leaf stage (1). The *xnt7.g* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Erbet (CIho 13826) (1).

Mutational events:

xnt7.g (GSHO 581) in Erbet (GSHO 2475) (1).

Mutant used for description and seed stocks:

xnt7.g (GSHO 581) in Erbet.

References:

1. Rahman, M.M. 1973. Balanced male sterile-lethals systems for hybrid barley production. Ph.D. Thesis. Montana State Univ., Bozeman.
2. Rahman, M.M., and R.F. Eslick. 1976. Linkage of spontaneous mutant seedling lethal genes with genetic male sterile genes. Barley Genet. Newsl. 6:53-58.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:231.

BGS 234, Multiovary 3, *mov3*

Stock number: BGS 234
Locus name: Multiovary 3
Locus symbol: *mov3*

Previous nomenclature and gene symbolization:

Multiovary = *mo-a* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 1H (2); based on linkage drag with the *Mla* (reaction to *Erysiphe graminis* a) locus (2).

Description:

Plants with the *mov3.h* gene have stamens converted into pistils. Stamen conversion ranges from a few stigma hairs at the top of one anther to three normal-looking pistils. Since most supernumerary pistils are non-functional, only one seed develops in each spikelet. In rare cases, the extra pistils form seeds having a very irregular shape and little endosperm. Since stamens with a few stigma hairs can shed pollen, about 17 percent of florets set seed under field conditions. Compared with other multiovary mutants (3, 4), plants with the *mov3.h* gene have normal or unconverted lodicules (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659) (2).

Mutational events:

mov3.h (OUM213) in Akashinriki (OUJ659) (2).

Mutant used for description and seed stocks:

mov3.h (OUM213) in Akashinriki (2).

Notes:

Tazhin mapped his *mo5* mutant very close to the *nud1* (naked caryopsis 1) locus (5). The two multiovary mutants studied by J. Soule, *mo6b* and *mo7a*, have been mapped to chromosomes 3HS and 7H, respectively (1). Since both *mo5* and *mo7a* are about 2 cM from the *nud* (naked caryopsis) locus, they are likely alleles. Thus, the third locus associated with multiovary trait is assigned the code *mov3* and the mutant allele at this locus is assigned the symbol *mov3.h* as the eighth multiovary mutant reported.

References:

1. Kleinhofs, A. 1999. Coordinator's report: Integrating barley molecular and morphological/physiological marker maps. Barley Genet. Newsl. 29:58-59.
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Prepared:

T. Konishi and J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:102.

BGS 235, Leafy lemma, *lel1*

Stock number: BGS 235
Locus name: Leafy lemma 1
Locus symbol: *lel1*

Previous nomenclature and gene symbolization:

Leafy lemma = *lel* (1).

Inheritance:

Monofactorial recessive, but a second gene *lel2* (probably *lks2*) is required for expression of leafy lemma phenotype (2).

Located in chromosome 1HL (2); about 6.1 cM distal from molecular marker MWG733 in bin 1H-12 (2).

Description:

The overall shape of the leafy lemma is similar to that of the typical grass leaf. The leafy lemma has a basal zone that is wider and more elongated, a transition zone, and a distal domain similar in shape to a leaf blade (1, 2). In all crosses analyzed, F₂ *lel1* plants always had awnless lemmas, the caryopsis was longer than normal and was partially naked, there was a tendency for the rachilla to bear more than one floret, and rachis internodes were elongated (2).

Origin of mutant:

A spontaneous mutant isolated at the Istituto Sperimentale per la Cerealicoltura (Fiorenzuola, Italy) in a plot of a recessive mutant for short awn, the *lks2* (short awn 2) line from the Small Grains Germplasm Research Facility (USDA-ARS), Aberdeen, Idaho (1, 2). The *lks2* gene is required for full expression of the leafy lemma phenotype (2).

Mutational events:

lel1.a in (GSHO 1780) G7118 (1, 2).

Mutant used for description and seed stocks:

lel1.a (GSHO 1780) in G7118; *lel1.a* in Bowman (PI 483237)*3 (GSHO 2279); *lel1.a* in Bowman*4 (BW474, NGB 20704).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
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Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:103.

BGS 238, Breviaristatum-t, *ari-t*

Stock number: BGS 238
Locus name: Breviaristatum-t
Locus symbol: *ari-t*

Previous nomenclature and gene symbolization:

Breviaristatum-25 = *ari-25* (3).

Inheritance:

Monofactorial recessive (2, 4).

Located in chromosome 1H (1); associated with SNP markers between 1_0744 to 1_1326 (positions 39.84 to 82.35 cM) in 1H bins 05 to 08 of the Bowman backcross-derived line BW032 (1).

Description:

The awns of *ari-t* plants are 2/3 of normal length and slightly curly. Peduncles are coiled and less than half normal length and plants are 1/2 to 2/3 normal height (4, 5). In the Bowman backcross-derived line BW032, leaf blades were shorter and narrower than those of Bowman. Kernels were shorter and narrower, seed weights were about 20% lower, and seed yields were about 1/4 of normal (2). A locus name was assigned based on the unique phenotype and lack of other breviaristatum mutants located in 1H.

Origin of mutant:

An ethylene oxide induced mutant in Bonus (PI 189763, NGB 14657) (4, 5).

Mutational events:

ari-t.25 (NGB 115673) in Bonus (PI 189763, NGB 14657) (5).

Mutant used for description and seed stocks:

ari-t.25 in Bonus (NGB 115673); *ari-t.25* in Bowman (PI 483237)*5 (BW032, NGB 20440).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å, A. Hagberg, U. Lundqvist and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.
5. Lundqvist, U. (Unpublished).

Prepared:

J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl. 40:82.

BGS 239, Scirpoides-b, *sci-b*

Stock number: BGS 239
Locus name: Scirpoides-b
Locus symbol: *sci-b*

Previous nomenclature and gene symbolization:

Scirpoides-1 = *sci-4* (3).

Inheritance:

Monofactorial recessive (2).

The location is limited to chromosomes 1H or 6H based on SNP markers retained in the Bowman backcross-derived line BW771, between 1_0259 to 2_0780 (positions 70.78 to 154.89 cM) in 1H and between 1_0061 and 2_0118 (positions 70.15 to 156.09 cM) in 6H (1).

Description:

Plants expressing the *sci-b* gene have narrow leaves and lower leaf blades are folded inward (4). In the Bowman backcross-derived line BW771, rachis internodes were slightly elongated. Plants were 2/3 to almost normal height, kernels were slightly smaller and lighter, and seed yields were about 3/4 of normal (2). Based on differences in morphology compared to the *sci-a* (scirpoides-a) mutants and different chromosomal segments retained in their Bowman backcross-derived lines (1), a new locus name is assigned.

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763, NGB 14657) (3).

Mutational events:

sci-b.4 (NGB 117099) in Bonus (PI 189763) (4).

Mutant used for description and seed stocks:

sci-b.4 (NGB 117099) in Bonus; *sci-b.4* in Bowman (PI 483237)*2 (BW771, NGB 22239).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Lundqvist, U. (Unpublished).

Prepared:

J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl 40:83.

BGS 240, Semidwarf 6, *sdw6*

Stock number: BGS 240
Locus name: Semidwarf 6
Locus symbol: *sdw6*

Previous nomenclature and gene symbolization:

Semidwarf f = *sdw.f* (2).

Inheritance:

Monofactorial recessive (4).

The location is limited to chromosomes 1H or 7H based on SNP markers retained in the Bowman backcross-derived line BW806, between 1_0764 to 1_0075 (positions 61.55 to 82.35 cM) in 1H and between 2_1270 and 1_1219 (positions 93.97 to 107.44 cM) in 7H (1).

Description:

Plants with the *sdw6.f* gene are 10 to 20% shorter than normal sibs in the Bowman backcross-derived line BW806. Kernels were slightly shorter and were 10 to 20% lighter. The number of kernels per spike was slightly reduced. Grain yields were about 3/4 of normal and test weights were slightly lower. Based on the heterogeneous marker positions in line BW806, *sdw6.f* is not an allele at any of the previously named semidwarf loci (1, 2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Vada (PI 243182) isolated as Betina (PI 362200) by Institute de la Recherche Agronomique, Versailles, Yvelines, France; released as a cultivar in 1970 (3, 4).

Mutational events:

sdw6.f (GSHO 2449, Betina) in Vada (PI 243182) (3).

Mutant used for description and seed stocks:

sdw6.f (GSHO 2449) in Vada; *sdw6.f* in Bowman (PI 483237)*4 (GSHO 2331), *sdw6.f* in Bowman*5 (BW806, NGB 20783).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Sigurbjörnsson, B., and A. Micke. 1974. Philosophy and accomplishments of mutation breeding. pp. 303-343. *In* Polyploidy and Induced Mutations in Plant Breeding. IAEA, Vienna.
4. USDA, GRIN. <http://www.ars-grin.gov/cgi-bin/npgs/acc/display.pl?1270981>.

Prepared:

J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:84.

BGS 241, Accordion rachis 3, *Acr3*

Stock number: BGS 241
Locus name: Accordion rachis 3
Locus symbol: *Acr3*

Previous nomenclature and gene symbolization:

Lax spike = Lax (7, 8)
Accordion rachis = *acr* (6).
Accordion rachis c = *acr.c* (4).
Accordion rachis 1 = *acr1.a* (5).

Inheritance:

Monofactorial incomplete dominant for lax spike, the third factor required for expression of accordion rachis 1 (*acr1*) trait (3, 4).

Located in chromosome 1HL (3); associated with SNP markers 2_1357 to 2_0997 (positions 76.96 to 94.86 cM) in 1HL of the Bowman backcross-derived lines BW009 and BW439 (3), likely in 1H bin 08. Bowman lines BW007, BW009, BW438 and BW456 contain overlapping segments of variable length and SNP marker patterns in 1H (3).

Description:

Plants have slightly elongated rachis internodes (1). The *Acr3* gene is in the third chromosomal region associated with expression of the accordion rachis trait in Bowman backcross derived lines BW009 and BW439. The contribution of the 1HL region to characteristics of the accordion phenotype is unknown. Only the line BW438 (*Lax.an* or *Acr3.an*) has a 1HL donor chromosome segment in a line lacking both the 2H and 4HL segments identified as containing the *acr1* (see BGS 097) and *Acr2* (see BGS 189) genes, respectively. Plants of the Bowman derived line BW438 lines were taller than Bowman and had slightly longer rachis internodes (4).

Origin of mutant:

A naturally occurring deviant for lax spike from several sources (3, 4).

Mutational events:

Acr3.a3 in ACBV89B229 (GSHO 1617) and ACBV89B232 (GSHO 1573) (3, 9); *Acr3.b3* in Burma Girl (CIho 14831, GSHO 1071) (4, 9); *Acr2.am2* and *Acr3.an* in AB 1398 [GSHO 1115, likely CIho 14785 from G.A. Wiebe (1)]. *Acr3.c3* in T188 (GSHO 1480) from R.W. Woodward (2).

Mutant used for description and seed stocks:

Acr3.a3 in ACBV89B229 (GSHO 1617); *Acr3.b3* in Burma Girl (GSHO 1071); *Acr2.am2* and *Acr3.an* in AB 1398 (CIho 14785); *Acr3.an* from AB 1398 in Bowman*5 (BW438, NGB 20670); *Acr3.b3* from Burma Girl in Bowman *2 (GSHO 1898); *Acr3.b3* in Bowman*5 (BW007, NGB 20415); *Acr32.am3* from AB 1398 in Bowman*4 (BW456, NGB 20688); *Acr3.a3* plus *acr1.a* and *Acr2.a2* in Bowman*7 (BW009, NGB 20417 and BW439, NGB 20671); *Acr3.c3* in T188 (GSHO 1480); *Acr3.c3* from T188 in Bowman*6 (BW008, NGB 20416).

References:

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2. Doney, D.L. 1961. An inheritance and linkage study of barley with special emphasis on purple pigmentation of the auricle. M.S. Thesis. Utah State Univ., Logan.
3. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic Dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
4. Franckowiak, J.D. (Unpublished).

5. Franckowiak J.D. 2001. BGS 97, Accordion rachis 1, *acr1*. Barley Genet. Newsl. 32:85.
6. Haus, T.E. 1957. Inheritance of rachis internode length and an abnormal rachis type in barley. Dissertation Abstr. 49:179-180.
7. Nilan, R.A. 1964. The cytology and genetics of barley, 1951-1962. Monogr. Suppl. 3, Res. Stud. Vol. 32, No. 1. Washington State Univ. Press, Pullman.
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Prepared:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:85-86.

BGS 242, Slender dwarf 6, *sld6*

Stock number: BGS 242
Locus name: Slender dwarf 6
Locus symbol: *sld6*

Previous nomenclature and gene symbolization:

Slender dwarf g = *sld.g* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 1H (1); associated with SNP markers 1_0259 to 1_0552 (positions 70.78 to 88.33 cM) in 1H and SNP markers 2_0226 to 2_0206 (positions 3.14 to 9.61 cM) in 5HS of the Bowman backcross-derived line BW854 (1), likely in 1H bins 07 or 08.

Description:

Plant height of the *sld6.g* mutant is reduced and leaf blades are much shorter and slightly narrower (2). Plants of the Bowman backcross-derived line BW854 were 15 to 25% shorter than those of Bowman and spikes had about 4 fewer fertile rachis nodes. Spikes were semi-compact with rachis internodes about 25% shorter than those of Bowman. Kernels of BW854 were shorter and slightly thinner than those of Bowman. Kernel weights and grain yields were about 3/4 of normal (3). Based on the heterogeneous SNP marker positions in BW954, *sld6.g* is not an allele at any of the previously named slender dwarf loci (1, 3).

Origin of mutant:

A sodium azide induced mutant in Glenn (CIho 15769) (2).

Mutational events:

sld6.g (GSHO 2482) in Glenn (CIho 15769) (2, 3).

Mutant used for description and seed stocks:

sld6.g (GSHO 2482) in Glenn; *sld6.g* in Bowman (PI 483237)*5 (GSHO 2355), *sld6.g* in Bowman*7 (BW854, NGB 22291).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
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3. Franckowiak, J.D. (Unpublished).

Prepared:

J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:87.

BGS 244, Dense spike 11, *dsp11*

Stock number: BGS 244
Locus name: Dense spike 11
Locus symbol: *dsp11*

Previous nomenclature and gene symbolization:

Dense spike am = *dsp.am* (2).
Dense spike an = *dsp.an* (2).
Dense spike ao = *dsp.ao* (2).

Inheritance:

Monofactorial incomplete dominant (2).
Located in chromosome 1HL (1); *dsp11.am* is associated with SNP markers 2_0798 to 1_0798 (positions 82.35 to 90.92 cM) in 1H bin 08 of the Bowman backcross-derived line BW260 (1); *dsp11.ao* is associated with SNP markers 2_1000 to 2_0956 (positions 76.28 to 98.23 cM) in 1H bins 08 to 09 of the Bowman backcross-derived line BW262 (1); *dsp11.an* is associated with SNP markers 1_0259 to 1_0466 (positions 70.78 to 119.29 cM) in 1H bins 07 to 10 of the Bowman backcross-derived line BW261 (1), likely in 1H bin 08.

Description:

All three Bowman backcross-derived lines with short rachis internodes were from crosses to Akashinriki and retained an overlapping region in 1HL. The line BW260 with *dsp11.am* was used for trait comparisons because other two lines also retained SNP markers on other chromosomes (1). In comparison to Bowman, plants of Bowman backcross-derived line BW260 were slightly shorter and had more compact spikes, rachis internode lengths 3.5 vs. 4.6 mm. Kernels were shorter, 8.6 vs. 9.7 mm, and about 10% lighter. Test weights were slightly lower and grain yields were about 3/4 those for Bowman. The other two Bowman backcross-derived lines in which the *dsp11* segment was retained, BW261 (*dsp11.an*) and BW262 (*dsp11.ao*) plants had slightly shorter rachis internodes and kernels than Bowman. Kernels were about 30% lighter and yields were lower. BW261 plants were slightly taller than Bowman plants while BW262 was shorter (2). A common chromosome segment of 6HL was retained in both BW261 and BW262, with the SNP markers overlapping in the region from 1_0645 to 1_1187 (positions 190.38 to 195.01 cM) in 6H bin 11 (1).

Origin of mutant:

Natural occurrence in Akashinriki (OUJ659, PI 467400) (2), extracted from an ethyl methanesulfonate induced mutant (OUM070) of Akashinriki (3, 4).

Mutational events:

dsp11.am (OUM070, GSHO 1722) in Akashinriki, *dsp11.an* (OUM105) in Akashinriki, *dsp11.ao* (OUM125, GSHO 1723) in Akashinriki (4).

Mutant used for description and seed stocks:

dsp11.am (OUM70, GSHO 1722) in Akashinriki; *dsp11.am* in Bowman (PI 483237)*4 (GSHO 2244), in Bowman*6 (BW260, NGB 22085); *dsp11.an* from Akashinriki in Bowman *4 (BW261, NGB 22086); *dsp11.ao* from Akashinriki in Bowman*6 (GSHO 2039), *dsp11.ao* in Bowman*8 (BW262, NGB 22087).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).

3. Konishi, T. 1970. Studies on EMS-induced mutation in barley III. Nogaku Kenkyu 53:141-152.

4. Konishi, T. 1975. Characteristics and inheritance of EMS-induced mutants in barley. Nogaku Kenkyu 55:53-56.

Prepared:

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:121-122.

BGS 251, Multiflorus 2, *mul2*

Stock number: BGS 251
Locus name: Multiflorus 2
Locus symbol: *mul2*

Previous nomenclature and gene symbolization:

Multiflorus 2 = *mlt2* (3).

The change to *mul2* was recommended by Robertson (2).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 6HL (1, 3); about 24.2 cM distal from the *rob1* (orange lemma 1) locus (1, 3).

Description:

Lateral spikelets may have supernumerary florets and occasionally nodal branches appear at random in the spike. The character shows variable expression in some crosses, and only a few spikes may be affected in some plants (3). The trait is expressed only as a malformed rachilla in some lateral spikelets of six-rowed plants in the Bowman backcross-derived line. The rachilla malformation is most pronounced near the middle of the spike and ranges from formation of a fertile floret to slight elongation of the rachilla. Confirmation that this trait is the same gene as in the original stock is not completed.

Origin of mutant:

A betatron induced mutant in Montcalm (CIho 7149) (3).

Mutational events:

mul2.b (Alb Acc 299, GBC326, GSHO 1394) in Montcalm (CIho 7149) (1, 3).

Mutant used for description and seed stocks:

mul2.b (GSHO 1394) in Montcalm; *mul2.b* plus *vrs1.a* in Bowman (PI 483237)*6 (GSHO 2089); *mul2.b* plus *vrs1.a* in Bowman*7 (BW 607, NGB 22173). (A six-rowed phenotype is required for expression.)

References:

1. Kasha, K.G., D.E. Falk, and A. Ho-Tsai. 1978. Linkage data with genes on chromosome 6. Barley Genet. Newsl. 8:61-65.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:154.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:232.

BGS 252, Early maturity 7, *eam7*

Stock number: BGS 252
Locus name: Early maturity 7
Locus symbol: *eam7*

Previous nomenclature and gene symbolization:

Early heading = *ec* (9).
Early maturity 7 = *ea7* (8).

Inheritance:

Monofactorial recessive (5, 8).
Located in chromosome 6HS (9); about 0.5 cM from the *rob1* (orange lemma 1) locus (8); about 3.0 cM from the centromere (7); *eam7.g* is associated with SNP markers 2_0886 to 1_0978 (positions 3.28 to 156.09 cM) in 6H bins 01 to 09 of the Bowman backcross-derived line BW288 (1); *eam7.g* is associated with homozygous SNP markers 2_0882 to 1_0615 (positions 6.19 to 28.27 cM) in 6H bins 01 to 02 of the Bowman backcross-derived line BW287 (1), likely in 6H bin 02.

Description:

Under short-day conditions in California, USA, mutant plants bloom about 4 weeks before California Mariout, produced relatively few tillers, were fine stemmed, and were relatively short. Differences were less pronounced under long-day conditions (8). Mutants were partially insensitive to photoperiod and have a vernalization requirement (9). Under long-day conditions, segregates expressing the *eam7.g* gene were difficult to identify (6). When the *Eam1.a* (early maturity 1) gene is not present, *eam7.g* plants headed 10 to 14 days earlier than Bowman in nurseries at Yuma, Arizona, USA, but only 3 to 5 days earlier at Fargo, North Dakota, USA. (2) The *Eam1.a* gene present in California Mariout apparently interacts with the *eam7.g* allele under short-day conditions to cause extreme earliness (2). The Bowman backcross lines for *eam7.g*, BW287 and 288, were 4 to 10 days earlier than Bowman under short days, but no differences were observed under long days (2). The *HvCO7* (*Hordeum vulgare* *CONSTANS 7*) gene was located on the same chromosome arm as *eam7* gene (5).

Origin of mutant:

A spontaneous mutant in Atlas (PI 539108) identified as Atsel (CIho 6250) (3); present in male sterile Club Mariout/6*California Mariout (PI 527380) (3, 9).

Mutational events:

eam7.g in BC₆ California Mariout (GBC326, GSHO 579) (4, 8); *eam7.n* (Ea1), *eam7.o* (Ea2), *eam7.p* (Ea3) in Chikurin Ibaraki 1 (OUJ069, CIho 7370) 10).

Mutant used for description and seed stocks:

eam7.g (GSHO 579) from Atsel in California Mariout (CIho 1455)*7; *eam7.g* in Bowman (PI 483237)*3 (GSHO 2068, BW288, NGB 205572), *eam7.g* in Bowman*2 (BW287, NGB 20571).

References:

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Prepared:

C.R. Burnham. 1971. *Barley Genet. Newsl.* 1:155. Early heading, *ea7*.

Revised:

J.D. Franckowiak and L.W. Gallagher. 1997. *Barley Genet. Newsl.* 26:233.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:123-124.

BGS 253, Uniculm 2, *cul2*

Stock number: BGS 253
Locus name: Uniculm 2
Locus symbol: *cul2*

Previous nomenclature and gene symbolization:

Uniculm 2 = *uc2* (8).

Inheritance:

Monofactorial recessive (8).

Located in chromosome 6HL (4, 6); about 1.3 cM distal from the *gsh4* (glossy sheath 4) locus (3, 5); about 11.4 cM from the *msg36* (male sterile genetic 36) locus (3, 5); about 2.2 cM proximal from the *rob1* (orange lemma 1) locus (3, 4, 5); about 8.8 cM from RFLP markers cMWG679 and ABG458 (1); about 6.2 cM from AFLP marker E4343-10 in subgroup 54 of the Proctor/Nudinka map (7).

Description:

The *cul2* plants have a single elongated culm (stem), the stem is much greater in diameter than normal, and plants are usually earlier than normal (8). The *cul2* plants initiate vegetative axillary meristems, but tillers fail to develop (1). Irregular placement of some spikelets and male fertility in lateral spikelets occur in the original stock (5) and in the Bowman backcross-derived line (1). Yield of unicum plants is not restored when grown under high plant populations (2). Double mutant combinations with most other mutants that affect tiller number resulted in a unicum vegetative phenotype (1).

Origin of mutant:

A thermal neutron induced mutant in Kindred (CIho 6969) (8).

Mutational events:

cul2.b (GBC379, CIho 115530, GSHO 531) in Kindred (CIho 6969) (5), *cul2.k* (*unc^k*) in an unknown cultivar from the Max-Planck-Institut für Züchtungsforschung (7).

Mutant used for description and seed stocks:

cul2.b (CIho 115530, GSHO 531) in Kindred; *cul2.b* in Bowman (PI 483237)*4 (GSHO 2074); *cul2.b* in Bowman*7 (BW205, NGB 22033); *cul2.b* plus *rob1.a* from sel 79Cal in Bowman*8 (GSHO 2075, BW206, NGB 22034).

References:

1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley unicum2 (*cul2*) mutant. Theor. Appl. Genet. 106:846–857.
2. Dofing, S.M. 1996. Near-isogenic analysis of unicum and conventional-tillering barley lines. p. 617-619. In A.E. Slinkard, G.J. Scoles, and B.G. Rosnagel (eds.) Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp., Saskatoon. Univ. of Saskatchewan, Saskatoon.
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4. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VI. Ten mutant genes located on chromosomes 1 to 7, except 3. Ber. Ohara Inst. landw. Biol., Okayama Univ. 18:227-250.
5. Kasha, K.G., D.E. Falk, and A. Ho-Tsai. 1978. Linkage data with genes on chromosome 6. Barley Genet. Newsl. 8:61-65.
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Prepared:

C.R. Burnham. 1971. Barley Genet. Newsl. 1:156.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:234.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:253-254.

BGS 254, Orange lemma 1, *rob1*

Stock number: BGS 254
Locus name: Orange lemma 1
Locus symbol: *rob1*

Previous nomenclature and gene symbolization:

Orange lemma = *pl* (14).
Orange lemma = *br* (1, 2).
Orange lemma = *o* (15).
Robiginosum-o = *rob-o* (6).

Inheritance:

Monofactorial recessive (1, 2, 14, 15).
Located in chromosome 6HS (4, 5, 17, 18); about 10.8 cM proximal from the *msg36* (male sterile genetic 36) locus (5, 9); and about 2.2 cM distal from the *cul2* (uniculm 2) locus (5, 7, 9); near RFLP marker HVM031 in 6H bin 06 (3).

Description:

The lemma, palea, and rachis have an orange pigmentation that is present in immature spikes, can be observed at heading, and is retained in mature grain and spikes (2, 15). The orange pigmentation is visible at the base of sheath of seedlings and in exposed nodes after jointing. Internodes have a layer of orange tissue and stems have an orange color as the straw dries. The mutant stock for *rob1.f* (OUM189) has a lighter orange lemma color than that in other mutants at the *rob1* locus (10). The Bowman backcross-derived line with the *rob1* gene had slightly lower acid-detergent lignin (ADL) content than Bowman (13), but it was also more susceptible to common root rot, caused by *Bipolaris sorokiniana* (11).

Origin of mutant:

A spontaneous mutant in CIho 5649 (15).

Mutational events:

rob1.a in CIho 5649 (GBC340, GSHO 707) (8, 15); *rob1.b* (OUM185), *rob1.c* (OUM186), *rob1.d* (OUM187), *rob1.e* (OUM188), *rob1.f* (OUM189) in Akashinriki (OUJ659, PI 467400) (10); *rob1.1* (NGB 115071, NGB 119367), *rob1.2* (NGB 115072, NGB 119368) in Bonus (PI 189763), *rob1.3* (NGB 115073, NGB 119369), *rob1.4* (NGB 115074, NGB 119370), *rob1.5* (NGB 115075, NGB 119371), *rob1.6* (NGB 115076, 119372) in Foma (CIho 11333), *rob1.7* (NGB 115077, NGB 119373) in Kristina (NGB 1500) (12); *rob1.g* (200A12/8/2) from Emir (CIho 11790) isolated following a cross to *Hordeum bulbosum* (16).

Mutant used for description and seed stocks:

rob1.a (GSHO 707) in CIho 5649; *rob1.a* in Bowman (PI 483237)*8 (GSHO 2069, BW666, NGB 20752).

References:

1. Bauman, A. 1926. Barley with orange lemmas. Bull. Appl. Bot. & Pl. Breed. 16:181-186.
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8. Ivanova, K.V. 1937. A new character in barley "third outer glume" — Its inheritance and linkage with color of the flowering glumes. *Bull. Appl. Bot., Genet. & Pl. Breed.* II. 7:339-353.
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13. Meyer, D.W., J.D. Franckowiak, and R.D. Nudell. 2006. Forage quality of barley hay. *Agronomy Abstracts* 2006.
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Prepared:

C.R. Burnham. 1971. *Barley Genet. Newsl.* 1:157.

Revised:

J.D. Franckowiak, T. Konishi, and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:235-236.
J.D. Franckowiak and U. Lundqvist. 2007. *Barley Genet. Newsl.* 37:255-256.

BGS 255, Xantha seedling 5, *xnt5*

Stock number: BGS 255
Locus name: Xantha seedling 5
Locus symbol: *xnt5*

Previous nomenclature and gene symbolization:

Yellow seedling (3).

Xantha seedling n = x_n (4).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 6HL (1, 5); about 25.0 cM distal from the *rob1* (orange lemma 1) locus (5); about 18.8 cM distal from the *lax-b* (laxatum-b) locus (2).

Description:

Seedlings have a pale yellow color and do not survive beyond the two or three leaf stage (1). The *xnt5.e* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Nepal (CIho 595) (3).

Mutational events:

xnt5.e (Nepal I, GSHO 43) in Nepal (CIho 595) (3).

Mutant used for description and seed stocks:

xnt5.e (GSHO 43) in Nepal.

References:

1. Kramer, H.H., and B.A. Swomley Blander. 1961. Orienting linkage maps on the chromosomes of barley. *Crop Sci.* 1:339-342.
2. Larsson, H.E.B. 1985. Linkage studies with genetic markers and some *laxatum* barley mutants. *Hereditas* 103:269-279.
3. Robertson, D.W. 1933. Inheritance in barley. *Genetics* 18:148-158.
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Prepared:

C.R. Burnham. 1971. *Barley Genet. Newsl.* 1:158.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:237.

BGS 257, Smooth awn 5, *raw5*

Stock number: BGS 257
Locus name: Smooth awn 5
Locus symbol: *raw5*

Previous nomenclature and gene symbolization:

Smooth awn e = $r_{,,e}$ (1).
Smooth awn 2 = r_2 (1).
Smooth awn 5 = r_5 (2).

Inheritance:

Monofactorial recessive (1).
Located in chromosome 6HL (1, 2); over 31.5 cM distal from the *rob1* (orange lemma 1) locus (3).

Description:

Plants have fewer stigma hairs and seed set is reduced, but more barbs developed on the central vein of the awn than in *raw1.a* plants (2). The Bowman backcross-derived line contains both of *raw1.a* and *raw5.e* genes for smooth awn. It has very smooth awns and very few stigma hairs, and seed set is often less than 10%.

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (1).

Mutational events:

raw5.e (OUM195, GSHO 771) in Akashinriki (OUJ659, PI 467400) (1, 2); *raw5.e* plus *rob1.a* in GSHO 785 (from T. Konishi).

Mutant used for description and seed stocks:

raw5.e (GSHO 771) in Akashinriki; *raw5.e* in Bowman (PI 483237)*6 (GSHO 2085, BW664, NGB 22472).

References:

1. Konishi, T. 1971. A new smooth awn gene on chromosome 6. Barley Genet. Newsl. 1:25-26.
2. Konishi, T. 1975. [Characteristics and inheritance of EMS-induced mutants.] Nogaku Kenkyu 55:53-66. [In Japanese.]
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Prepared:

T. Konishi. 1976. Barley Genet. Newsl. 6:131.

Revised:

T. Konishi and J. D. Franckowiak. 1997. Barley Genet. Newsl. 26:238.

BGS 258, Dense spike 9, *dsp9*

Stock number: BGS 258
Locus name: Dense spike 9
Locus symbol: *dsp9*

Previous nomenclature and gene symbolization:

Dense spike = *la* (1).
Dense spike 9 = *l9* (1).

Inheritance:

Monofactorial recessive (1).
Located in chromosome 6HL (1); about 27.2 cM distal from the *xnt5* (xantha seedling 5) locus (2); over 26.9 cM distal from the *Aat2* (aspartate aminotransferase 2) locus (4).

Description:

Extremely dense spikes are easily distinguished from normal types when grown in the field or greenhouse (1). The spike often emerges from the side of the sheath. Yield and seed size are reduced somewhat in the Bowman backcross-derived line.

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (1).

Mutational events:

dsp9.i (OUM113, GSHO 1774) in Akashinriki (OUJ659, PI 467400) (1); *dsp9.j* (OUM106), *dsp9.k* (OUM107), *dsp9.l* (OUM115), *dsp9.m* (OUM118) in Akashinriki (3).

Mutant used for description and seed stocks:

dsp9.i (GSHO 1774) in Akashinriki; *dsp9.i* in Bowman (PI 483237)*7 (GSHO 2090, BW279, NGB 20563).

References:

1. Konishi, T. 1973. Genetic analyses of EMS-induced mutants in barley. Barley Genet. Newsl. 3:28-31.
2. Konishi, T. 1978. New linkage data on chromosome 6 of barley. Barley Genet. Newsl. 8:71-72.
3. Konishi, T. (Unpublished).
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Prepared:

T. Konishi. 1976. Barley Genet. Newsl. 6:132.

Revised:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:239.

BGS 260, Chlorina seedling 11, *fch11*

Stock number: BGS 260
Locus name: Chlorina seedling 11
Locus symbol: *fch11*

Previous nomenclature and gene symbolization:

Pale green = *pg* (2).
Chlorina seedling 11 = *f11* (1).

Inheritance:

Monofactorial recessive (2).
Located in chromosome 6HL (3); about 6.1 cM distal from the *rob1* (orange lemma 1) locus (2, 3).

Description:

Seedlings are pale yellow-green and often have white blotches on the seedling leaves. Plants remain light green until maturity (2). Plant vigor is good, but plant developmental stages are delayed.

Origin of mutant:

An X-ray induced mutant in Himalaya (CIho 1312) obtained by Caldecott and North at the University of Minnesota (1).

Mutational events:

fch11.t (GBC357 and GBC359, GSHO 1738) in Himalaya (CIho 1312) (1).

Mutant used for description and seed stocks:

fch11.t (GSHO 1738) in Himalaya; *fch11.t* in Bowman (PI 483237)*6 (GSHO 2082); *fch11.t* in Bowman*7 (BW353, NGB 20592).

References:

1. Burnham, C.R., and K.J. Kasha. 1979. BGS 260, Chlorina seedling, *f11*. Barley Genet. Newsl. 9:133.
2. Falk, D.E., and K.J. Kasha. 1979. The map location of a pale green mutant on chromosome 6. Barley Genet. Newsl. 9:17-18.
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Prepared:

C.R. Burnham and K.J. Kasha. 1979. Barley Genet. Newsl. 9:133.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:240.

BGS 261, Necrotic leaf spot 2, *nec2*

Stock number: BGS 261
Locus name: Necrotic leaf spot 2
Locus symbol: *nec2*

Previous nomenclature and gene symbolization:

Mutant no 7 (1).
Necrotic leaf spots 2 = *nec2b* (2).

Inheritance:

Monofactorial recessive (1).
Located in chromosome 6HS (1); about 5.2 cM from the *rob1* (orange lemma 1) locus (3).

Description:

Small, dark brown necrotic spots appear on the leaves of field grown plants 3 to 6 weeks after germination. Margins of the spots have poor demarcation, and the expression of necrotic spot is not good some years (3).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Carlsberg II (CIho 10114) (1).

Mutational events:

nec2.b (Mutant no 7, GSHO 1224), *nec2.c* (Mutant no 9) in Carlsberg II (CIho 10114) (1).

Mutant used for description and seed stocks:

nec2.b (GSHO 1224) in Carlsberg II.

References:

1. Jensen, J. 1971. Mapping of 10 mutant genes for necrotic spotting in barley by means of translocations. p. 213-219. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
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Prepared:

J. Jensen. 1981. *Barley Genet. Newsl.* 11:102.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:241.

BGS 262, Curly 1, *cur1*

Stock number: BGS 262
Locus name: Curly 1
Locus symbol: *cur1*

Previous nomenclature and gene symbolization:

Curly 1 = *cu1* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 6HL (2); over 31.5 cM distal from the *rob1* (orange lemma 1) locus (3); not linked to *rob1* (1).

Description:

All plant parts appear curved or twisted. Lemmas and awns are extremely curly. The rachis is usually bent, and tillers are curved or wavy (3).

Origin of mutant:

The origin is unknown.

Mutational events:

cur1.a (Alb Acc 23, G395, GSHO 1705) in 48-cr cr-17 (3).

Mutant used for description and seed stocks:

cur1.a (GSHO 1705) in 48-cr cr-17; *cur1.a* in Bowman (PI 483237)*4 (GSHO 2088); *cur1.a* in Bowman*4 (BW219, NGB 22046) [The *cur1.a* mutant stock in Bowman (BW219, NGB 22046) is likely an allele at the *cur2* locus.]

References:

1. Kasha, K.G., D.E. Falk, and A. Ho-Tsai. 1978. Linkage data with genes on chromosome 6. Barley Genet. Newsl. 8:61-65.
2. Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement III. 1954-1963. Crop Sci. 5:33-43.
3. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:242.

BGS 263, Curly 3, *cur3*

Stock number: BGS 263
Locus name: Curly 3
Locus symbol: *cur3*

Previous nomenclature and gene symbolization:

Curly 3 = *cu3* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 6HL (5); about 22.9 cM distal from the *cul2* (uniculm 2) locus (4, 5); *cur3.e* is associated with SNP markers 2_0488 to 1_1147 (positions 119.40 to 137.78 cM) in 6H bins 07 to 08 of the Bowman backcross-derived line BW222 (1), likely in 6H bin 08.

Description:

Stem internodes are curved in a bow-like manner and awns are slightly coiled (5). Seedlings elongate rapidly and leaves are nearly twice as long as normal. Seedlings homozygous for the *cur3.e* allele do not show additional elongation in response to gibberellic acid treatment (3). Plants of the Bowman backcross-derived line for *cur3.e*, BW222, had an open crown semi-prostrate early growth and were about 15% shorter than Bowman. Kernels of BW222 were slightly small and weighed 5 to 10% less. The grain yields of BW222 were about 3/4 those of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Akashinriki (OUJ659, PI 467400) isolated by A. Yamashita (5).

Mutational events:

cur3.e (OUM301, GSHO 1707) in Akashinriki (OUJ659, PI 467400) (4, 5).

Mutant used for description and seed stocks:

cur3.e (GSHO 1707, OUM301) in Akashinriki; *cur3.e* in Bowman (PI 483237)*6 (GSHO 2087), in Bowman*7 (BW222, NGB 22049).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:243.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:125.

BGS 264, Mottled leaf 5, *mtt5*

Stock number: BGS 264
Locus name: Mottled leaf 5
Locus symbol: *mtt5*

Previous nomenclature and gene symbolization:

Mottled f = *mt*,,f (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 6HL (3); about 6.4 cM distal from the *rob1* (orange lemma 1) locus (3); *mtt5.f* is associated with SNP markers 2_0936 to 2_0577 (positions 71.39 to 117.10 cM) in 6H bins 06 to 07 of the Bowman backcrossed-derived line BW603 (1), likely in 6H bin 07.

Description:

Mottled bands occur on the leaf blade and sheath and are retained until heading (3). The first few seedling leaves often do not show the mottled trait. Plants of Bowman backcross-derived line for *mtt5.f*, BW603, were less vigorous than Bowman and heading was slightly delayed. BW603 had slightly lower kernel weights and grain yields ranging from 1/2 to 3/4 those of Bowman (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (3).

Mutational events:

mtt5.f (OUM022, GSHO 2410) in Akashinriki (OUJ659, PI 467400) (3).

Mutant used for description and seed stocks:

mtt5.f (GSHO 2410, OUM022) in Akashinriki; *mtt5.f* in Bowman (PI 483237)*6 (GSHO 2084); *mtt5.f* in Bowman*7 (BW603, NGB 22169).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Konishi, T. 1978. New linkage data on chromosome 6 of barley. *Barley Genet. Newsl.* 8:71-72.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:244.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:126.

BGS 265, Necrotic leaf spot 3, *nec3*

Stock number: BGS 265
Locus name: Necrotic leaf spot 3
Locus symbol: *nec3*

Previous nomenclature and gene symbolization:

Necrotic leaf spot 3 = *nec3a* (2, 3, 6).

Necrotic leaf spot 3 = *nec3b* (3, 6).

Inheritance:

Monofactorial recessive (2, 5).

Located in chromosome 6HS (2, 5); about 29.2 cM distal from the *rob1* (orange lemma 1) locus (1, 2, 4); about 16.7 cM distal from the *msg36* (male sterile genetic 36) locus (1).

Description:

Tan or brown necrotic blotches develop on the leaf sheath and blade prior to heading and persist to maturity (2, 3). Plants homozygous for *nec3.d* develop brown blotches having irregular margins. Plants homozygous for *nec3.e* develop large tan or faded blotches having distinct margins. After maturation, plants expressing the *nec3.d* gene can be identified easily by brown blotches on the leaves, but those expressing the *nec3.e* gene are difficult to identify. In the Bowman backcross-derived lines, vigor is reduced more in *nec3.e* plants than in *nec3.d* ones.

Origin of mutant:

An X-ray induced mutant in Proctor (PI 280420) (2, 5).

Mutational events:

nec3.d (1339/62, GSHO 1330) in Proctor (PI 280420) (2, 5); *nec3.e* (1558/74, GSHO 2423) in Villa (PI 399506) (3).

Mutant used for description and seed stocks:

nec3.d (GSHO 1330) in Proctor; *nec3.e* (GSHO 2423) in Villa; *nec3.d* in Bowman (PI 483237)*4 (GSHO 2065); *nec3.d* in Bowman*6 (BW629, NGB 22195); *nec3.e* in Bowman*3 (GSHO 2066); *nec3.e* in Bowman*6 (BW630, NGB 22196).

References:

1. Falk, D.E., M.J. Swartz, and K.J. Kasha. 1980. Linkage data with genes near the centromere of barley chromosome 6. Barley Genet. Newsl. 10:13-16.
2. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
3. Fischbeck, G., and H. Häuser. 1978. Cytogenetic studies of some induced barley mutants. Barley Genet. Newsl. 8:36-37.
4. Häuser, H., and G. Fischbeck. 1980. Genetic analysis of induced mutations. Barley Genet. Newsl. 10:30-31.
5. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.
6. Søgaard, B., and P. von Wettstein-Knowles. 1987. Barley: genes and chromosomes. Carlsberg Res. Comm. 52:123-196.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:245.

BGS 266, Erectoides-e, *ert-e*

Stock number: BGS 266
Locus name: Erectoides-e
Locus symbol: *ert-e*

Previous nomenclature and gene symbolization:

Erectoides-17 = *ert-17* (2).
Dense spike = *la* (4).
Dense spike 9 = *l9* (4).

Inheritance:

Monofactorial recessive (2, 4, 8).
Located in chromosome 6HL (3, 7, 8); about 27.2 cM distal from the *xnt5* (xantha seedling 5) locus (3); over 26.9 cM distal from the *Aat2* (aspartate aminotransferase 2) locus (11).

Description:

Spikes are very compact with rachis internode length values from 1.2 to 1.5 mm. Plants are about 2/3 normal height. Partial fertility and reduced vigor are noted among *ert-e* mutants. The peduncle is very short and spikes often emerge from the side of the flag sheath (7, 9). A large deficiency of mutant plants is frequently noted in segregating populations (7). Spike density decreases greatly when plants are treated with GA₃ as the flag leaf emerges (10). The mutant *ert-e.17* is allelic to mutant *dsp9.i* (dense spike 9, see BGS 258) (1).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (2).

Mutational events:

ert-e.17 (GSHO 477, NGB112619), -e.65 (NGB 112664) in Bonus (PI 189763) (2); *ert-e.94* (NGB 112693), -e.143 (NGB 112742) in Bonus, -e.331 (NGB112846), -e.396 (NGB 114150) in Foma (CIho 11333) (9); *dsp9.i* (OUM113) in Akashinriki (4); *dsp9.j* (OUM106), *dsp9.k* (OUM107), *dsp9.l* (OUM115), *dsp9.m* (OUM118, GSHO 1774) in Akashinriki (6).

Mutant used for description and seed stocks:

ert-e.17 (GSHO 477, NGB 112619) in Bonus; *ert-e.17* in Bowman (PI 483237)*6 (GSHO 2091); *ert-e.17* in Bowman*7 (BW307, NGB 22103); *dsp9.i* (GSHO 1774) in Akashinriki; *dsp9.i* in Bowman (PI 483237)*7 (GSHO 2090, BW279, NGB 20563).

References:

1. Franckowiak, J.D. (Unpublished).
2. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
3. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
4. Konishi, T. 1973. Genetic analyses of EMS-induced mutants in barley. *Barley Genet. Newsl.* 3:28-31.
5. Konishi, T. 1978. New linkage data on chromosome 6 of barley. *Barley Genet. Newsl.* 8:71-72.
6. Konishi, T. (Unpublished).
7. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. *Hereditas* 62:25-96.
8. Persson, G., and A. Hagberg. 1962. Linkage studies with the erectoides loci. *Barley Newsl.* 5:46-47.

9. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.
10. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. *Hereditas* 58:359-384.
11. Yoshimi, R., and T. Konishi. 1995. Linkage analysis of several isozyme loci in barley. *Barley Genet. Newsl.* 24:35-37.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:246.

Revised as BGS 258:

T. Konishi and J.D. Franckowiak. 1997. BGS 258, Dense spike 9, *dsp9*. *Barley Genet. Newsl.* 26:239.

Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:257-258.

BGS 267, Reaction to *Puccinia hordei* 11, *Rph11*

Stock number: BGS 267
Locus name: Reaction to *Puccinia hordei* 11 (barley leaf rust)
Locus symbol: *Rph11*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Located in chromosome 6HL (1); about 7.0 cM proximal from the *Acp3* (acid phosphatase 3) locus; about 11.0 cM proximal from the *Dip2* (dipeptidase 2) locus (1).

Description:

The seedling reaction varies from a necrotic fleck to a moderate sized uredinium with heterozygotes having an intermediate reaction (1). Culture Aust 220 from Australia is required to detect a resistant reaction in allelism tests and backcrosses. Seedlings tend to show a moderate sized uredinium as a reaction to many isolates of *Puccinia hordei*.

Origin of mutant:

Natural occurrence in accession 'Maalot 17' of *Hordeum vulgare* subsp. *spontaneum*, but isolated as a Clipper backcross-derived line containing one of two *Rph* genes in the original accession (1).

Mutational events:

Rph11.p (BC67, GSHO 1589) from *Hordeum vulgare* subsp. *spontaneum* in Clipper*4/Maalot 17 (1).

Mutant used for description and seed stocks:

Rph11.p (BC67, GSHO 1589) in Clipper*4/Maalot 17; *Rph11.p* in Bowman (PI 483237)*2 (GSHO 2092); *Rph11.p* in Bowman*6 (PI 643160, BW684, NGB 22390).

References:

1. Feuerstein, U., A.H.D. Brown, and J.J. Burdon. 1990. Linkage of rust resistance genes from wild barley (*Hordeum spontaneum*) with isozyme markers. Plant Breed. 104:318-324.

Prepared:

J.D. Franckowiak and Y. Jin. 1997. Barley Genet. Newsl. 26:247.

BGS 268, Laxatum-b, *lax-b*

Stock number: BGS 268
Locus name: Laxatum-b
Locus symbol: *lax-b*

Previous nomenclature and gene symbolization:

Laxatum-1 = *lax-1* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 6HL (3); about 27.3 cM distal from the *rob1* (orange lemma 1) locus (3); about 18.8 cM proximal from the *xnt5* (xantha seedling 5) locus (3).

Description:

Plants are weak and short (3/4 normal), spikes are lax and spikelet number is reduced. Seeds are small and thin and have a shrunken endosperm (xenia), which is detectable in the heterozygous condition (2). Treatment of leaves after tillering with GA₃ increases rachis internode length (5). Seed set is reduced in the Bowman backcross-derived line.

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (4).

Mutational events:

lax-b.1 (NGB 116335, GSHO 1776) in Bonus (PI 189763) (2).

Mutant used for description and seed stocks:

lax-b.1 (NGB 116335, GSHO 1776) in Bonus; *lax-b.1* in Bowman (PI 483237)*7 (GSHO 2083, BW459, NGB 20690).

References:

1. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
2. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. *Hereditas* 103:239-253.
3. Larsson, H.E.B. 1985. Linkage studies with genetic markers and some *laxatum* barley mutants. *Hereditas* 103:269-279.
4. Lundqvist, U. (Unpublished).
5. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. *Hereditas* 58:359-384.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:248.

BGS 269, High lysine 6, *lys6*

Stock number: BGS 269
Locus name: High lysine 6
Locus symbol: *lys6*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1, 2).
Located in chromosome 6H (2).

Description:
At the hard dough stage, kernels homozygous for the *lys6.i* gene develop a depression near the center of the lemma, which becomes progressively more distinct as the kernels mature. Mutant plants produce grain that has a 12% increase in lysine content (1). Shrunken endosperm and high lysine content have a pleiotropic association in stocks homozygous for the *lys6.i* gene (1, 2).

Origin of mutant:
A gamma-ray induced mutant in Bomi (PI 43371) (1).

Mutational events:
lys6.i (Risø 527, GSHO 1786) in Bomi (PI 43371) (1, 3).

Mutant used for description and seed stocks:
lys6.i (GSHO 1786) in Bomi; *lys6.i* in Bowman (PI 483237)*3 (GSHO 2077), *lys6.i* in Bowman*6 (BW498, NGB 20726).

References:
1. Doll, H. 1976. Genetic studies of high lysine barley mutants. p. 542-546. *In* H. Gaul (ed.) Barley Genetics III. Proc. Third Int. Barley Genet. Symp., Garching, 1975. Verlag Karl Thieme, München.
2. Jensen, J. 1979. Chromosomal location of one dominant and four recessive high-lysine genes in barley mutants. Vol. 1. p. 89-96. *In* Seed Protein Improvement in Cereals and Grain Legumes. Proc. Int. Symp., Neuherberg, Germany, 1978. Int. Atomic Energy Agency, Vienna.
3. Jensen, J., and H. Doll. 1979. Gene symbols for barley high-lysine mutants. Barley Genet. Newsl. 9:33-37.

Prepared:
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:249.

BGS 270, Albino seedling 14, *abo14*

Stock number: BGS 270
Locus name: Albino seedling 14
Locus symbol: *abo14*

Previous nomenclature and gene symbolization:

Albino seedling f = *alb,,f* (3).

Albino seedling q = *alb,,q* (4).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 6HL (1, 2); about 12.5 cM distal from the *rob1* (orange lemma 1) locus (2); about 8.1 cM distal from the *sex1* (shrunken endosperm xenia 1) locus (1).

Description:

Seedlings have a white color and die at the two to three leaf stage (3). The *abo14.q* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Shabet (CIho 13827) (3).

Mutational events:

abo14.q (G365, GSHO 586) in Shabet (CIho 13827) (3, 4).

Mutant used for description and seed stocks:

abo14.q (GSHO 586) in Shabet.

References:

1. Falk, D.E., M.J. Swartz, and K.J. Kasha. 1980. Linkage data with genes near the centromere of barley chromosome 6. Barley Genet. Newsl. 10:13-16.
2. Kasha, K.J., D.E. Falk, and A. Ho-Tsai. 1978. Linkage data with genes on chromosome 6. Barley Genet. Newsl. 8:61-65.
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4. Rahman, M.M., and R.F. Eslick. 1976. Linkage of spontaneous mutant seedling lethal genes with genetic male sterile genes. Barley Genet. Newsl. 6:53-58.

Prepared:

J.D. Franckowiak and D.E. Falk. 1997. Barley Genet. Newsl. 26:250.

BGS 271, Albino seedling 15, *abo15*

Stock number: BGS 271
Locus name: Albino seedling 15
Locus symbol: *abo15*

Previous nomenclature and gene symbolization:

Albino seedling t = *alb*,,t (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 6HS (1, 2); over 28.9 cM distal from the *msg6* (male sterile genetic 6) locus (2); over 39.0 cM distal from the *rob1* (orange lemma 1) locus (2).

Description:

Seedlings have a white color and die at the two to three leaf stage (1). The *abo15.t* gene must be maintained as a heterozygous stock.

Origin of mutant:

A diethyl sulfate induced mutant in a stock of Betzes (PI 129430) that was trisomic for chromosome 6 (1).

Mutational events:

abo15.t in Betzes trisomic for chromosome 6 (1).

Mutant used for description and seed stocks:

abo15.t in Betzes trisomic for chromosome 6.

References:

1. Clark, D.R., and R.T. Ramage. 1976. An induced albino mutation on chromosome 6. Barley Genet. Newsl. 6:8-9.
2. Falk, D.E., M.J. Swartz, and K.J. Kasha. 1980. Linkage data with genes near the centromere of barley chromosome 6. Barley Genet. Newsl. 10:13-16.

Prepared:

J.D. Franckowiak and D.E. Falk. 1997. Barley Genet. Newsl. 26:251.